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Remarks:
The applicant has subsequently filed a sequence listing and declared, that it includes no new matter.

(54) Novel LDL receptor analog protein and the gene coding therefor

(57) The present invention is drawn to the gene of a novel LDL receptor family receptor which participates in lipoprotein metabolism, a critical factor that triggers the onset of arteriosclerosis.

The invention provides DNA having a nucleotide sequence as shown by Sequence ID No. 1 or No.5 is disclosed as well as rabbit tissue or human tissue LDL receptor analog protein having an amino acid sequence of Sequence ID No. 2 or 6 coded by such DNA.

EP 0 773 290 A2

Description

Background of the Invention:

5   1) Field of the Invention

The present invention relates to a novel LDL receptor analog protein having a structure similar to that of LDL receptors that are responsible for the homeostasis mechanism of intracellular cholesterol and extensively participates in serum lipid metabolism, which is a critical factor that triggers the onset of arteriosclerosis. The invention also relates to
10 the gene coding for the protein.

2) Description of the Related Art

Abnormality in serum lipid metabolism is one of the most critical risk factors in the onset and progress of arterio-
15 sclerosis. Serum lipids, together with apolipoproteins, are transformed into lipoproteins primarily in the liver, secreted therefrom, transported by blood, and taken up by a variety of tissue cells.

Uptake of lipoproteins into cells occurs primarily by the mediation of receptors of respective lipoproteins. It is known that low density lipoproteins (LDL), which are taken into cells by specific membrane receptors, called LDL receptors, are metabolized within the cells and utilized as cell membrane components or similar substances. Detailed analysis of
20 familial hyperchlolesterolemia, which is a genetic disease accompanied by notable hyperchlolesterolemia due to abnor-mality of LDL receptors, has clarified details of the mechanism of homeostasis achieved by LDL receptors with respect to intracellular cholesterol.

It has been suggested that living bodies have not only LDL receptors but also cell membrane receptors that recog-nize other lipoproteins. From analyses of WHHL rabbits, which are model animals lacking LDL receptors, it was found
25 that receptors which takes principally apo-E-containing lipoproteins as ligands (remnant receptors) are present in the liver. It is also predicted that there may be HDL receptors whose ligands are high density lipoprotein (HDL). However, to date, details of the structures and functions of these receptors have not yet been elucidated. It has also been known that foaming of macrophages plays an active role in the formation of atherosclerosis, is deeply participated. Macro-phages foam by taking up modified LDL —not normal LDL— which have undergone oxidation, acetylation, or glycation.
30 There have recently been discovered receptors to modified LDL which are called scavenger receptors. The scavenger receptors have been identified to be membrane receptors that have a structure completely different from that of LDL receptors.

Recent research using molecular biological techniques has identified the genes of LRP (LDL receptor-associated protein), gp 330, and VLDL receptors. The receptors have been found to have structures very similar to those of LDL
35 receptors. From analyses of these receptors, it is believed that a plurality of lipoprotein receptors are present in living bodies, and that they are closely related to lipid metabolism. LDL receptors studied in detail by Brown and Goldstein [Brown, M.S. and Goldstein, J.L. (1986) Science 232, 34-47] are known to play an important role in the homeostasis of lipoprotein metabolism *in vivo*, recognizing apo-B-100 and apo-E and taking primarily LDL as their ligands. Also, LRP, which is a macroprotein, has been found to primarily recognize apo-E and to take β-VLDL or chylomicron remnant as
40 a ligand. Moreover, it has been recently reported that LRP takes an α_2-macroglobulin/protease complex or a plasmino-gen activator/plasminogen activator inhibitor-1 complex as a ligand, and that LRP is a protein identical to the α_2-mac-roglobulin receptor. When these findings are taken together, LRP is considered to have a wide variety of functions in living bodies [Herz, J., Hamann, U., Rogne, S., Myklebost, O., Gausepohl, H. and Stanley, K.K. (1989) EMBO J. 7(13), 4119-4127; Brown, M.S., Herz, J., Kowal, R.C. and Goldstein, J.L. (1991) Current Opinion in Lipidology 2, 65-72; Herz,
45 J. (1993) Current Opinion in Lipidology 4, 107-113]. The gp 330, which was first identified as an antigen inducing rat Heymann nephritis, has been reported to have a ligand-binding capacity similar to that possessed by CRP α_2-mac-roglobulin receptor [Raychowdhury, R., Niles, J.L., McCluskey, R.T. and Smith, J.A. (1989) Science 244, 1163-1165; Pietromonaco, S., Kerjaschki, D., Binder, S., Ullrich, R. and Farquhar, G. (1990) Proc. Natl. Acad. Sci. U.S.A. 87, 1811-1815]. In addition, recently discovered VLDL receptors, which are found to take VLDL as a ligand, are considered to
50 have new functions including fatty acid metabolism, because they are predominantly found in tissues of the heart and muscles though they are rarely found in the liver [Takahashi, S., Kawarabayashi, Y., Nakai, T., Sakai, J. and Yamamoto, T. (1992) Proc. Natl. Acad. Sci. USA 89, 9252-9256].

Functions of these newly found receptors as lipoprotein receptors have been gradually elucidated through detailed *in vitro* analyses. However, significance of respective receptors in living bodies has mostly been left unknown. In addi-
55 tion, relations to remnant receptors, HDL receptors, etc., which have conventionally been identified or suggested by bio-chemical techniques, remain unknown. Presently, it is considered that these newly found receptors are products of genes different from those of the latter receptors. Thus, more lipoprotein receptors than originally guessed have become considered to participate in lipoprotein uptake into cells while interacting with each other to thereby function to maintain homeostasis of lipid metabolism in living bodies. However, from structural analyses of the genes of the afore-

mentioned newly-identified receptors, it is predicted that the genes of these receptors that take lipoproteins as ligands are developed from the same gene from which LDL receptors was developed, and thus they are within the same genetic family. This suggests that lipoprotein receptors that have conventionally been proposed may have structures similar to those of LDL receptors.

5   Accordingly, an object of the present invention is to provide the gene of a novel receptc r in the LDL receptor family, as well as a protein coded by the gene.

The present inventors conducted careful studies so as to attain the above object, and found that by using part of rabbit LDL receptor cDNA as a probe there can be obtained a DNA fragment coding for a peptide having a structure similar to that of LDL receptors. Moreover, when using part of the obtained cDNA as a probe, a cDNA fragment having

10   a sequence similar to that of the cDNA can be obtained from the human tissue cDNA library. The present invention was accomplished based on these findings.

Summary of the Invention

15   The present invention provides DNA having a nucleotide sequence shown by Sequence ID No. 1 or No. 5; an LDL receptor analog protein having an amino acid sequence coded by the DNA; a recombinant vector comprising the DNA and a replicable vector; transformant cells which harbor the recombinant vector; and a method for the production of the LDL receptor analog protein.

20   Description of Preferred Embodiment

The cDNA of the present invention may be prepared, for example, by the following process.

Briefly, the process includes the following steps. (1) Through the use of rabbit LDL receptor cDNA as a probe, positive clones are screened out of a rabbit liver cDNA library. (2) Recombinant DNA is prepared using the separated pos-

25   itive clones, and a cDNA fragment is cut out of the resultant recombinant DNA through a treatment using a restriction enzyme The cDNA fragment is integrated into a plasmid vector. (3) Host cells are transformed using the obtained cDNA recombinant vector to thereby obtain transformant cells of the present invention. The obtained transformant cells are incubated so as to obtain a recombinant vector containing a DNA fragment of the present invention. The nucleotide sequence of the DNA fragment of the present invention contained in the resultant recombinant vector is determined. (4)

30   In tissue of a living body, there is detected expression of mRNA indicated by the nucleotide sequence of the cDNA of the present invention by using RNA blot hybridization method. (5) Through use of a rabbit cDNA fragment as a probe, positive clones are screened out of a human tissue cDNA library, and the nucleotide sequence of the clones is determined. (6) A recombinant vector for expression is prepared using the cDNA of the present invention. Through use of the thus-obtained vector, host cells are transformed to thereby obtain the transformants of the present invention. (7) Lig-

35   ands that are bound to protein expressed by the obtained transformants are detected by ligand blotting.

Each of the above-described steps will next be described.

(1) Screening for positive clones from a rabbit liver cDNA library:

40   · A cDNA library may be prepared by the use of mRNA obtained from rabbit liver, reverse transcriptase, and a suitable vector, e.g., commercially available λgt10 vector.

A cDNA library thus prepared using λgt10 as a vector is subjected to a screening for positive clones by the application of a DNA hybridization method employing a cDNA probe, to thereby separate positive clones [Sambrook, J., Fritsch, E.F. and Maniatis, T. (1989) In: Molecular Cloning: A Laboratory Manual, pp 9.47-9.58, Cold Spring Harbor Lab-

45   oratory Press].

An exemplary cDNA which may be used as a probe is rabbit LDL receptor cDNA. Positive clones may be detected by autoradiography employing a DNA probe labelled with a radioisotope (^{32}P).

(2) Preparation of a cDNA recombinant vector:

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Recombinant vector λgt10 phage DNA is extracted from the isolated positive clones and purified. The resultant purified recombinant vector λgt10 phage DNA is digested with a restriction enzyme EcoRI, to thereby separate a cDNA fragment from the vector DNA. The obtained cDNA fragment is integrated with a plasmid vector for cloning that has been similarly digested with EcoRI, thereby obtaining a recombinant plasmid vector. An exemplary plasmid vector

55   which may be used is pBluescript II.

(3) Recombinant vector, transformation of host cells using the recombinant vector, and preparation of DNA:

The obtained cDNA recombinant vector is introduced into a variety of host cells that are capable of utilizing the

genetic marker possessed by the recombinant vector, to thereby transform the host cells. Host cells are not particularly limited, with *E. coli* being preferred. For example, a variety of variants of the *E. coli* K12 strain, e.g., HB-101, may be used. In order to introduce the recombinant vector into host cells, a competent cell method may be used in combination with a treatment with calcium.

5   The thus-obtained transformant cells are cultured in a selective medium in accordance with the genetic marker of the vector. The recombinant vector of the present invention is collected from the cultured cells. The DNA nucleotide sequence of the cDNA contained in the obtained recombinant vector can be determined through use of a dideoxy sequence method [Sanger, F., Nicklen, S. and Coulson, A.R. (1977) Proc. Natl. Acd. Sci. USA 74, 5463-5467].

10   (4) RNA blot hybridization:

The expression in tissue of mRNA, indicated by the nucleotide sequence of the cDNA of the present invention, is detected using RNA blot hybridization.

First, mRNA is prepared using rabbit tissue. Commercially available oligo(dT)cellulose column may be used for the
15   preparation. In order to prepare mRNA from human tissue, there may be used a commercially available nylon membrane on which tissue poly(A)$^+$RNA from a variety of sources is present.

An exemplary probe is the rabbit cDNA obtained in the above-described step (3). mRNA may be detected by autoradiography employing a DNA probe labelled with a radioisotope (^{32}P).

20   (5) Screening of human tissue cDNA library for positive clones, and determination of nucleotide sequence:

An exemplary human tissue cDNA library which may be used is a commercially available human brain cDNA library.

Screening and nucleotide sequencing of the human brain cDNA library may be performed using a fragment of rab-
25   bit cDNA of the present invention as a probe in a manner similar to that used for the aforementioned rabbit liver cDNA library.

(6) Preparation of a recombinant vector for expression and transformation of host cells using the recombinant vector for expression:
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In order to prepare an LDL receptor analog protein through use of cDNA of the present invention, the obtained cDNA and a vector for expression are first bonded to each other to thereby create a recombinant vector for expression. Vectors for expression which may be used for bonding are not particularly limited. For example, pBK-CMV may be used.

Host cells are transformed using the thus-obtained recombinant vector for expression, to thereby obtain a trans-
35   formant cell of the present invention. The obtained transformant cell is cultured so as to obtain cells that are capable of expressing the protein of the invention. Host cells are not particularly limited. For example, CHO cells may be used. In order to introduce the recombinant vector for expression into host cells, a calcium phosphate method may be used.

The thus-prepared transformant cells are incubated in a selective medium in accordance with the genetic marker of the vector, so as to express the LDL receptor analog protein of the present invention.
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(7) Ligand analysis of the protein by ligand blotting:

After the resultant transformant cells are incubated, the expressed LDL receptor analog protein is solubilized using a solubilizer, e.g., Triton X-100, to thereby obtain a membrane protein fraction. The fraction is separated using SDS-
45   PAGE, and transferred onto, for example, a nitrocellulose membrane. Using a radio-labelled (^{125}I) lipoprotein as a probe, the analog protein can be detected by autoradiography. Exemplary lipoproteins which may be used include β-VLDL and LDL.

Examples:
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The present invention will next be described in detail by way of example, which should not be construed as limiting the invention.

Example 1:
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Preparation of a rabbit liver cDNA library:

From tissue of the liver of a male Japanese white rabbit, intact RNA was extracted through a guanidium thiocyanate/cesium chloride method. The obtained intact RNA was subjected to an oligo (dT) cellulose column method to

thereby obtain purified poly(A)+RNA.

cDNA was synthesized in accordance with a method of Gubler and Hoffman [Gubler, U. and Hoffman, B.J. (1983) Gene 25, 263]. Briefly, cDNA was synthesized employing rabbit liver poly(A)+RNA (as a template), a random primer, and moloney murine leukemia virus reverse transcriptase. The synthesized cDNA was transformed into double-

5   stranded DNA using DNA polymerase I, and then subjected to an EcoRI methylase treatment. By the use of T4 DNA polymerase, the DNA was blunt-ended. The blunt-ended DNA was ligated to phosphorylated EcoRI linker pd (CCGAATTCGG) using a T4 DNA ligase, and the resultant ligated product was subjected to an additional digestion with EcoRI. cDNA fragments having a size not less than 1 kb were selected by agarose gel electrophoresis, and integrated into the EcoRI-digested site of λgt10 phage DNA using a T4 DNA ligase. The phage DNA was packaged in vitro, to

10 thereby establish a rabbit liver cDNA library.

Example 2:

Cloning of cDNA of receptors in the rabbit LDL receptor family:

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The cDNA library (1,000,000 plaques) prepared in Example 1 was subjected to screening using a plaque hybridization method and employing as a probe a segment of the cDNA obtained from a ligand binding region, the functional region, of the rabbit LDL receptor. Hybridization was performed at 42°C using 5 x SSC, 30% formamide, 1% SDS, 5 x Denhardt's, and 100 μg/ml salmon sperm DNA (ssDNA), followed by washing with 0.3 x SSC/0.1% SDS at 48°C. As a

20 result, several positive clones were obtained. These cDNA clones were separated by performing this plaque hybridization method in a plurality of times. Subsequently, a cDNA fragment of each phage was subcloned into a plasmid vector pBluescript II, and the nucleotide sequence was analyzed using a dideoxy sequence method [Sanger, F., Nicklen, S. and Coulson, A.R. (1977) Proc. Natl. Acd. Sci. USA 74, 5463-5467]. Based on a putative amino acid sequence, LDL receptors themselves were excluded, and cDNA clones having a sequence very similar to that of LDL receptors were

25 identified. Using these clones as cDNA probes, the cDNA library was screened to thereby obtain overlapping two clones. These were employed as new probes and similar procedure was performed, so as to obtain 5 cDNA clones. The DNA nucleotide sequence determined by these cDNA clones are shown as Sequence ID No. 3. The total length of the sequence was 6961 bp. In the open reading frame of 6639 bp (Sequence ID No. 1) which contained a sequence exhibiting high homology with LDL receptors, there existed on the 5' side an ATG codon which was presumably a translation

30 initiating site and a successive highly hydrophobic sequence consisting of about 30 amino acids. Accordingly, the obtained cDNA was considered to contain the entirety of its length. A putative amino acid sequence is shown as Sequence ID No. 2. The protein consisted of 2213 amino acids. Comparison of the amino acid sequence of the protein with other amino acid sequence data registered at the Genebank, there was a very high similarity to LDL receptors. That is, amino acids 700 - 1,100 in the sequence were very similar to the EGF precursor homology region of LDL recep-

35 tors, and amino acids 1,100 - 1,640 were also very similar to the ligand binding region of LDL receptors. When the amino acid sequence of the subject protein was compared with other lipoprotein receptor LRP, gp330, and VLDL receptors, similarity was not as high as that observed for LDL receptors. On the C-terminal side of the amino acid sequence of the protein, there was found a highly hydrophobic region which was very similar to the transmembrane region of LDL receptors.

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Example 3:

From liver tissue and brain tissue of a male Japanese white rabbit, intact RNA was extracted through a guanidium thiocyanate/cesium chloride method. The obtained intact RNA was subjected to an oligo (dT) cellulose column method

45 to thereby obtain purified poly(A)+RNA. The poly(A)+RNA specimens (10 μg each) was modified via a glyoxal method, electrophoresed on 1% agarose gel, and transferred onto a nylon membrane.

For human tissue mRNA, commercially available nylon membranes blotted with human tissue poly(A)+RNA from various sources were used.

Using as a probe part of a ^{32}P-labelled rabbit cDNA of the present invention, hybridization was performed at 42°C

50 using 50% (rabbit) or 40% (human) formamide, 0.1% SDS, 50 mM phosphate buffer, 5 x Denhardt's, 5 x SSC, and 200 μg/ml of ssDNA, followed by washing with 0.1 x SSC and 0.1% SDS at 50°C. Autoradiography was performed at -70°C for 2 days in the presence of intensifying screen. As a result, in both rabbit liver tissue and brain tissue, mRNA of about 7 kb was detected as well as mRNA of about 15 kb which was considered to result from alternative splicing or polyadenylation. The size of the mRNA of about 7 kb coincided with that of the rabbit cDNA of the present invention. Also, in

55 human liver tissue and brain tissue, it was confirmed that mRNA having the same size was expressed.

Example 4:

Screening of human brain cDNA library for positive clones and determination of the nucleotide sequence of cDNA fragments

The human brain cDNA library used in this Example was a commercially obtained cDNA library which was constructed using λgt10 as a vector. Using partial cDNA of the present invention as a probe, screening of the cDNA library (300,000 plaques) was performed using a plaque hybridization method. Procedures of screening, cloning, and sequencing were as described in Example 2 of the present invention.

As a result of screening of the human brain cDNA library, positive clones containing a DNA fragment of about 3 kb were obtained. Analysis of the nucleotide sequence of part of the cDNA fragment revealed that the fragment was highly homologous to the cDNA of the present invention (Sequence ID No. 4).

Example 5:

Cloning of cDNA of receptors in the human LDL receptor family:

A human brain cDNA library was subjected to screening using fragments of the cDNA of the present invention and fragments of the cDNA obtained in Example 4 as probes. Procedures of screening, cloning, and sequencing were as described in Example 2 of the present invention.

Through screening of the human brain cDNA library, two positive clones containing cDNA fragments of about 6 kb and about 3 kb were obtained. When their nucleotide sequence was analyzed, they were identified to be a cDNA clone containing the cDNA nucleotide sequence obtained in Example 4 and a cDNA clone that overlapped therewith. Using part of these cDNAs as probes, procedures similar to those as described above were performed, to thereby obtain another cDNA clone The DNA nucleotide sequence indicated by these cDNA clones are shown as Sequence ID No. 7. The total length of the sequence was 6,843 bp. There was an open reading frame having a size of 6,642 bp (Sequence ID No. 5). A putative amino acid sequence is shown as Sequence ID No. 6. The protein consisted of 2,214 amino acids. Comparison of the amino acid sequence with that of rabbit protein shown by Sequence ID No. 2 revealed high homology of not less than 94%.

Example 6:

Creation of cells that express receptors in the rabbit LDL receptor family:

The cDNA as shown by Sequence ID No. 3 was ligated to phosphorylated EcoRI linker pd (CCGAATTCGG) by the use of a T4 DNA ligase, and the resultant ligated product was digested with EcoRI. Separately, a vector for expression, pBK-CMV was digested with EcoRI. The aforementioned DNA was ligated to the EcoRI-digested site of the vector using a T4 DNA ligase.

Using the resultant recombinant expression vector in a calcium phosphate method [Chen, C. and H. Okayama (1987) Mol. Cell. Biol. 7, 2745-2752], host cells (CHO-1d1A7) were transformed. The resultant transformants were incubated in a Ham's F-12 selective medium supplemented with 500 μg/ml of G418, and viable cells were separated as LDL receptor analog protein-expressing cells. The cells were incubated further in the aforementioned medium.

Example 7:

Ligand analysis of the LDL receptor analog protein by ligand blotting:

The obtained LDL receptor analog protein-expressing cells and control cells were suspended in a buffer solution containing 200 mM Tris-maleic acid (pH 6.5), 2 mM calcium chloride, 0.5 mM PMSF, 2.5 μM leupeptin, and 1% Triton X-100, to thereby solubilize the membrane protein. Solubilized membrane protein fractions were obtained through centrifugation, and electrophoresed by a 4.5-18% gradient SDS-PAGE. Thereafter, the protein was transferred onto a nitrocellulose membrane.

Incubation was performed in a buffer of 50 mM Tris-HCl (pH 8.0) containing ^{125}I-labelled β-VLDL (10 μg/ml), 2 mM calcium chloride, and 5% bovine serum albumin. Autoradiography was performed at room temperature.

A single band of about 250 kDa was detected in membrane protein fractions prepared using the present protein-expressing cells. This size coincided well with the molecular weight of 248 kDa calculated regarding the amino acid sequence (Sequence ID No. 2) deduced from the cDNA of the present invention. Although a similar band was detected for control cells, the expression level was much lower as compared with the case of the present protein-expressing cells.

Since the protein coded by the cDNA of the present invention is considered to be a novel LDL receptor family recep-

tor, it is expected that through analyses of this protein, details of lipoprotein metabolism mediated by the membrane receptor will be elucidated, and pathology of abnormal lipid metabolism which triggers onset and progress of arteriosclerosis will be clarified.

Sequence ID No. 1

Length of the Sequence: 6639

Type: nucleic acid

Strandedness: double

Topology: linear

Molecular type: cDNA to mRNA

Sequence:

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ATGGCGACAC GGAGCAGCAG GAGGGAGTCG CGACTCCCCT TCCTATTCAC CCTGGTCGCG    60

CTGCTGCCGC CCGGGGCTCT CTGCGAGGTG TGGACGCGGA CACTGCACGG CGGCCGCGCG   120

CCCTTACCCC AGGAGCGGGG CTTCCGCGTG GTGCAGGGCG ACCCGCGCGA GCTGCGGCTG   180

TGGGAGCGCG GGGATGCCAG GGGGGCGAGC CGGGCGGACG AGAAGCCGCT CCGGAGGAGA   240

CGGAGCGCTG CCCTGCAGCC CGAGCCCATC AAGGTGTACG GACAGGTCAG CCTCAATGAT   300

TCCCACAATC AGATGGTGGT GCACTGGGCC GGAGAGAAAA GCAACGTGAT CGTGGCCTTG   360

GCCCGGGACA GCCTGGCGTT GGCCAGGCCC AGGAGCAGTG ATGTGTACGT GTCTTATGAC   420

TATGGAAAAT CATTCAATAA GATTTCAGAG AAATTGAACT TCGGCGCGGG AAATAACACA   480

GAGGCTGTGG TGGCCCAGTT CTACCACAGC CCTGCGGACA ACAAACGGTA CATCTTCGCA   540

GATGCCTACG CCCAGTATCT CTGGATCACG TTTGACTTCT GCAACACCAT CCATGGCTTT   600

TCCATCCCGT TCCGGGCAGC TGATCTCCTA CTCCACAGTA AGGCCTCCAA CCTTCTCCTG   660

CGCTTCGACA GGTCTCACCC CAACAAGCAG CTGTGGAAGT CGGATGATTT TGGCCAGACC   720

TGGATCATGA TTCAAGAACA CGTGAAGTCC TTTTCTTGGG GAATTGATCC CTATGACAAA   780

CCAAACACCA TCTACATCGA ACGGCACGAA CCTTCTGGCT ACTCCACGGT TTTCCGAAGT   840

ACAGACTTCT TCCAGTCCCG GGAAAACCAG GAAGTGATCT TGGAGGAAGT GAGAGACTTT   900

CAGCTTCGGG ACAAGTACAT GTTTGCTACA AAGGTGGTGC ATCTCTTGGG CAGTCCACTG   960

CAGTCTTCTG TCCAGCTCTG GGTCTCCTTT GGCCGGAAGC CCATGCGGGC CGCCCAGTTT  1020

GTTACAAGAC ATCCTATCAA CGAATATTAC ATCGCGGATG CCTCGGAGGA CCAGGTGTTT  1080

GTGTGTGTCA GTCACAGCAA CAACCGCACC AACCTCTACA TCTCGGAGGC AGAGGGCTTG  1140

AAGTTCTCTC TGTCCCTGGA GAACGTGCTC TACTACACCC CGGGAGGGGC CGGCAGTGAC  1200

ACCTTGGTGA GGTACTTTGC AAATGAACCG TTTGCTGACT TCCATCGTGT GGAAGGGTTG  1260
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CAGGGAGTCT ACATTGCTAC TCTGATTAAT GGTTCTATGA ATGAGGAGAA CATGAGATCT    1320

GTCATCACCT TTGACAAAGG GGGCACCTGG GAATTTCTGC AGGCTCCAGC CTTCACGGGG    1380

TATGGAGAGA AAATCAACTG TGAGCTGTCC GAGGGCTGTT CCCTCCACCT GGCCCAGCGC    1440

CTCAGCCAGC TGCTCAACCT CCAGCTCCGG AGGATGCCCA TCCTGTCCAA GGAGTCGGCG    1500

CCTGGCCTCA TCATTGCCAC GGGCTCAGTG GGAAAGAACT TGGCTAGCAA GACAAACGTG    1560

TACATCTCTA GCAGTGCTGG AGCCAGGTGG CGAGAGGCAC TTCCTGGACC TCACTACTAT    1620

ACATGGGGAG ACCATGGCGG CATCATCATG GCCATTGCCC AAGGCATGGA AACCAACGAA    1680

CTGAAGTACA GTACCAACGA AGGGGAGACC TGGAAAGCCT TCACCTTCTC TGAGAAGCCC    1740

GTGTTTGTGT ATGGGCTCCT CACGGAACCC GGCGAGAAGA GCACGGTCTT CACCATCTTT    1800

GGCTCCAACA AGGAGAACGT GCACAGCTGG CTCATCCTCC AGGTCAATGC CACAGACGCC    1860

CTGGGGGTTC CTTGCACAGA GAACGACTAC AAGCTCTGGT CACCATCTGA TGAGCGGGGG    1920

AATGAGTGTT TGCTTGGACA CAAGACTGTT TTCAAACGGA GGACCCCGCA CGCCACATGC    1980

TTTAACGGAG AAGACTTTGA CAGGCCGGTG GTTGTGTCCA ACTGCTCCTG CACCCGGGAG    2040

GACTATGAGT GTGACTTTGG CTTCCGGATG AGTGAAGACT TGGCATTAGA GGTGTGTGTT    2100

CCAGATCCAG GATTTTCTGG AAAGTCCTCC CCTCCAGTGC CTTGTCCCGT GGGCTCTACG    2160

TACAGGCGAT CAAGAGGCTA CCGGAAGATT TCTGGGGACA CCTGTAGTGG AGGAGATGTT    2220

GAGGCACGGC TAGAAGGAGA GCTGGTCCCC TGTCCCCTGG CAGAAGAGAA CGAGTTCATC    2280

CTGTACGCCA CGCGCAAGTC CATCCACCGC TATGACCTGG CTTCCGGAAC CACGGAGCAG    2340

TTGCCCCTCA CTGGGTTGCG GGCAGCAGTG GCCCTGGACT TTGACTATGA GCACAACTGC    2400

CTGTATTGGT CTGACCTGGC CTTGGACGTC ATCCAGCGCC TCTGTTTGAA CGGGAGTACA    2460

GGACAAGAGG TGATCATCAA CTCTGACCTG GAGACGGTAG AAGCTTTGGC TTTTGAACCC    2520

CTCAGCCAAT TACTTTACTG GGTGGACGCA GGCTTTAAAA AGATCGAGGT AGCCAATCCA    2580

GATGGTGACT TCCGACTCAC CGTCGTCAAT TCCTCGGTGC TGGATCGGCC CCGGGCCCTG    2640

GTCCTTGTGC CCCAAGAAGG GATCATGTTC TGGACCGACT GGGGAGACCT GAAGCCTGGG    2700

ATTTATCGGA GCAACATGGA CGGATCTGCC GCCTATCGCC TCGTGTCGGA GGATGTGAAG    2760

TGGCCCAATG GCATTTCCGT GGACGATCAG TGGATCTACT GGACGGATGC CTACCTGGAC    2820

TGCATTGAGC GCATCACGTT CAGCGGCCAG CAGCGCTCCG TCATCCTGGA CAGACTCCCG    2880

CACCCCTATG CCATTGCTGT CTTTAAGAAT GAGATTTACT GGGATGACTG GTCACAGCTC    2940
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AGCATATTCC GAGCTTCTAA GTACAGCGGG TCCCAGATGG AGATTCTGGC CAGCCAGCTC   3000

ACGGGGCTGA TGGACATGAA GATCTTCTAC AAGGGGAAGA ACACAGGAAG CAATGCGTGT   3060

GTACCCAGGC CGTGCAGCCT GCTGTGCCTG CCCAGAGCCA ACAACAGCAA AAGCTGCAGG   3120

TGTCCAGATG GCGTGGCCAG CAGTGTCCTC CCTTCCGGGG ACCTGATGTG TGACTGCCCT   3180

AAGGGCTACG AGCTGAAGAA CAACACGTGT GTCAAAGAAG AAGACACCTG TCTGCGCAAC   3240

CAGTACCGCT GCAGCAACGG GAACTGCATC AACAGCATCT GGTGGTGCGA TTTCGACAAC   3300

GACTGCGGAG ACATGAGCGA CGAGAAGAAC TGCCCTACCA CCATCTGCGA CCTGGACACC   3360

CAGTTCCGTT GCCAGGAGTC TGGGACGTGC ATCCCGCTCT CCTACAAATG TGACCTCGAG   3420

GATGACTGTG GGACAACAG TGACGAAAGG CACTGTGAAA TGCACCAGTG CCGGAGCGAC   3480

GAATACAACT GCAGCTCGGG CATGTGCATC CGCTCCTCCT GGGTGTGCGA CGGGGACAAC   3540

GACTGCAGGG ACTGGTCCGA CGAGGCCAAC TGCACAGCCA TCTATCACAC CTGTGAGGCC   3600

TCCAACTTCC AGTGCCGCAA CGGGCACTGC ATCCCCCAGC GGTGGGCGTG TGACGGCGAC   3660

GCCGACTGCC AGGATGGCTC TGATGAGGAT CCAGCCAACT GTGAGAAGAA GTGCAACGGC   3720

TTCCGCTGCC CGAACGGCAC CTGCATTCCC TCCACCAAGC ACTGTGACGG CCTGCACGAT   3780

TGCTCGGACG GCTCCGACGA GCAGCACTGC GAGCCCCTGT GTACACGGTT CATGGACTTC   3840

GTGTGTAAGA ACCGCCAGCA GTGCCTCTTC CACTCCATGG TGTGCGATGG GATCATCCAG   3900

TGCCGTGACG GCTCCGACGA GGACCCAGCC TTTGCAGGAT GCTCCCGAGA CCCCGAGTTC   3960

CACAAGGTGT GCGATGAGTT CGGCTTCCAG TGTCAGAACG GCGTGTGCAT CAGCTTGATC   4020

TGGAAGTGCG ACGGGATGGA TGACTGCGGG GACTACTCCG ACGAGGCCAA CTGTGAAAAC   4080

CCCACAGAAG CCCCCAACTG CTCCCGCTAC TTCCAGTTCC GGTGTGACAA TGGCCACTGC   4140

ATCCCCAACA GGTGGAAGTG TGACAGGGAG AATGACTGTG GGGACTGGTC CGACGAGAAG   4200

GACTGTGGAG ATTCACATGT ACTTCCGTCT ACGACTCCTG CACCCTCCAC GTGTCTGCCC   4260

AATTACTACC GCTGCGGCGG GGGGGCCTGC GTGATAGACA CGTGGGTTTG TGACGGGTAC   4320

CGAGATTGCG CAGATGGATC CGACGAGGAA GCCTGCCCCT CGCTCCCCAA TGTCACTGCC   4380

ACCTCCTCCC CCTCCCAGCC TGGACGATGC GACCGATTTG AGTTTGAGTG CCACCAGCCA   4440

AAGAAGTGCA TCCCTAACTG GAGACGCTGT GACGGCCATC AGGATTGCCA GGATGGCCAG   4500

GACGAGGCCA ACTGCCCCAC TCACAGCACC TTGACCTGCA TGAGCTGGGA GTTCAAGTGT   4560

GAGGATGGCG AGCCCTGCAT CGTGCTGTCA GAACGCTGCG ACGGCTTCCT GGACTGCTCA   4620
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GATGAGAGCG ACGAGAAGGC CTGCAGTGAT GAGTTAACTG TATACAAAGT ACAGAATCTT  4680

CAGTGGACAG CTGACTTCTC TGGGAATGTC ACTTTGACCT GGATGCGGCC CAAAAAAATG  4740

CCCTCTGCTG CTTGTGTATA CAACGTGTAC TATAGAGTTG TTGGAGAGAG CATATGGAAG  4800

ACTCTGGAGA CTCACAGCAA TAAGACAAAC ACTGTATTAA AAGTGTTGAA ACCAGATACC  4860

ACCTACCAGG TTAAAGTGCA GGTTCAGTGC CTGAGCAAGG TGCACAACAC CAATGACTTT  4920

GTGACCTTGA GAACTCCAGA GGGATTGCCA GACGCCCCTC AGAACCTCCA GCTGTCGCTC  4980

CACGGGGAAG AGGAAGGTGT GATTGTGGGC CACTGGAGCC CTCCCACCCA CACCCACGGC  5040

CTCATTCGCG AATACATTGT AGAGTATAGC AGGAGTGGTT CCAAGGTGTG GACTTCAGAA  5100

AGGGCTGCTA GTAACTTTAC AGAAATAAAG AACTTGTTGG TCAACACCCT GTACACCGTC  5160

AGAGTGGCTG CGGTGACGAG TCGTGGGATA GGAAACTGGA GCGATTCCAA ATCCATTACC  5220

ACCGTGAAAG GAAAAGCGAT CCCGCCACCA AATATCCACA TTGACAACTA CGATGAAAAT  5280

TCCCTGAGTT TTACCCTGAC CGTGGATGGG AACATCAAGG TGAATGGCTA TGTGGTGAAC  5340

CTTTTCTGGG CATTTGACAC CCACAAACAA GAGAAGAAAA CCATGAACTT CCAAGGGAGC  5400

TCAGTGTCCC ACAAAGTTGG CAATCTGACA GCACAGACGG CCTATGAGAT TTCCGCCTGG  5460

GCCAAGACTG ACTTGGGCGA TAGTCCTCTG TCATTTGAGC ATGTCACGAC CAGAGGGGTT  5520

CGCCCACCTG CTCCTAGCCT CAAGGCCAGG GCTATCAATC AGACTGCAGT GGAATGCACC  5580

TGGACAGGCC CCAGGAATGT GGTGTATGGC ATTTTCTATG CCACATCCTT CCTGGACCTC  5640

TACCGCAACC CAAGCAGCCT GACCACGCCG CTGCACAACG CAACCGTGCT CGTCGGTAAG  5700

GATGAGCAGT ATCTGTTTCT GGTCCGGGTG GTGATGCCCT ACCAAGGGCC GTCCTCGGAC  5760

TACGTGGTCG TGAAGATGAT CCCGGACAGC AGGCTTCCTC CCCGGCACCT GCATGCCGTT  5820

CACACCGGCA AGACCTCGGC CGTCATCAAG TGGGAGTCGC CCTACGACTC TCCTGACCAG  5880

GACCTGTTCT ATGCGATCGC AGTTAAAGAT CTGATACGAA AGACGGACCG GAGCTACAAA  5940

GTCAAGTCCC GCAACAGCAC CGTGGAGTAC ACCCTGAGCA AGCTGGAGCC CGGAGGGAAA  6000

TACCACGTCA TTGTGCAGCT GGGGAACATG AGCAAAGATG CCAGTGTGAA GATCACCACC  6060

GTTTCGTTAT CGGCACCCGA TGCCTTAAAA ATCATAACAG AAAATGACCA CGTCCTTCTC  6120

TTCTGGAAAA GTCTAGCTCT AAAGGAAAAG TATTTTAACG AAAGCAGGGG CTACGAGATA  6180

CACATGTTTG ATAGCGCCAT GAATATCACC GCATACCTTG GGAATACTAC TGACAATTTC  6240

TTTAAAATTT CCAACCTGAA GATGGGTCAC AATTACACAT TCACGGTCCA GGCACGATGC  6300
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CTTTTGGGCA GCCAGATCTG CGGGGAGCCT GCCGTGCTAC TGTATGATGA GCTGGGGTCT   6360
GGTGGCGATG CGTCGGCGAT GCAGGCTGCC AGGTCTACTG ATGTCGCCGC CGTGGTGGTG   6420
CCCATCCTGT TTCTGATACT GCTGAGCCTG GGGGTCGGGT TTGCCATCCT GTACACGAAG   6480
CATCGGAGGC TGCAGAGCAG CTTCACCGCC TTCGCCAACA GCCACTACAG CTCCAGACTC   6540
GGCTCCGCCA TCTTCTCCTC TGGGGATGAC TTGGGGGAGG ATGATGAACA TGCTCCTATG   6600
ATCACTGGAT TTTCGGACGA CGTCCCCATG GTGATAGCC                          6639
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Sequence ID No. 2

Length of the Sequence: 2213

Type: amino acid

Topology: linear

Molecular type: Protein

Sequence:

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Met Ala Thr Arg Ser Ser Arg Arg Glu Ser Arg Leu Pro Phe Leu Phe
                  5                 10                  15
Thr Leu Val Ala Leu Leu Pro Pro Gly Ala Leu Cys Glu Val Trp Thr
                 20                 25                  30
Arg Thr Leu His Gly Gly Arg Ala Pro Leu Pro Gln Glu Arg Gly Phe
                 35                 40                  45
Arg Val Val Gln Gly Asp Pro Arg Glu Leu Arg Leu Trp Glu Arg Gly
             50                 55                  60
Asp Ala Arg Gly Ala Ser Arg Ala Asp Glu Lys Pro Leu Arg Arg Arg
 65                 70                 75                  80
Arg Ser Ala Ala Leu Gln Pro Glu Pro Ile Lys Val Tyr Gly Gln Val
                 85                 90                  95
Ser Leu Asn Asp Ser His Asn Gln Met Val Val His Trp Ala Gly Glu
                100                105                 110
Lys Ser Asn Val Ile Val Ala Leu Ala Arg Asp Ser Leu Ala Leu Ala
                115                120                 125
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Arg Pro Arg Ser Ser Asp Val Tyr Val Ser Tyr Asp Tyr Gly Lys Ser
     130   135   140

Phe Asn Lys Ile Ser Glu Lys Leu Asn Phe Gly Ala Gly Asn Asn Thr
145   150   155   160

Glu Ala Val Val Ala Gln Phe Tyr His Ser Pro Ala Asp Asn Lys Arg
          165   170   175

Tyr Ile Phe Ala Asp Ala Tyr Ala Gln Tyr Leu Trp Ile Thr Phe Asp
          180   185   190

Phe Cys Asn Thr Ile His Gly Phe Ser Ile Pro Phe Arg Ala Ala Asp
          195   200   205

Leu Leu Leu His Ser Lys Ala Ser Asn Leu Leu Leu Gly Phe Asp Arg
     210   215   220

Ser His Pro Asn Lys Gln Leu Trp Lys Ser Asp Asp Phe Gly Gln Thr
225   230   235   240

Trp Ile Met Ile Gln Glu His Val Lys Ser Phe Ser Trp Gly Ile Asp
          245   250   255

Pro Tyr Asp Lys Pro Asn Thr Ile Tyr Ile Glu Arg His Glu Pro Ser
          260   265   270

Gly Tyr Ser Thr Val Phe Arg Ser Thr Asp Phe Phe Gln Ser Arg Glu
          275   280   285

Asn Gln Glu Val Ile Leu Glu Glu Val Arg Asp Phe Gln Leu Arg Asp
     290   295   300

Lys Tyr Met Phe Ala Thr Lys Val Val His Leu Leu Gly Ser Pro Leu
305   310   315   320

Gln Ser Ser Val Gln Leu Trp Val Ser Phe Gly Arg Lys Pro Met Arg
          325   330   335

Ala Ala Gln Phe Val Thr Arg His Pro Ile Asn Glu Tyr Tyr Ile Ala
          340   345   350

Asp Ala Ser Glu Asp Gln Val Phe Val Cys Val Ser His Ser Asn Asn
  355   360   365

Arg Thr Asn Leu Tyr Ile Ser Glu Ala Glu Gly Leu Lys Phe Ser Leu
  370   375   380

Ser Leu Glu Asn Val Leu Tyr Tyr Thr Pro Gly Gly Ala Gly Ser Asp
385   390   395   400

Thr Leu Val Arg Tyr Phe Ala Asn Glu Pro Phe Ala Asp Phe His Arg
     405   410   415

Val Glu Gly Leu Gln Gly Val Tyr Ile Ala Thr Leu Ile Asn Gly Ser
     420   425   430

Met Asn Glu Glu Asn Met Arg Ser Val Ile Thr Phe Asp Lys Gly Gly
  435   440   445

Thr Trp Glu Phe Leu Gln Ala Pro Ala Phe Thr Gly Tyr Gly Glu Lys
  450   455   460

Ile Asn Cys Glu Leu Ser Glu Gly Cys Ser Leu His Leu Ala Gln Arg
465   470   475   480

Leu Ser Gln Leu Leu Asn Leu Gln Leu Arg Arg Met Pro Ile Leu Ser
     485   490   495

Lys Glu Ser Ala Pro Gly Leu Ile Ile Ala Thr Gly Ser Val Gly Lys
     500   505   510

Asn Leu Ala Ser Lys Thr Asn Val Tyr Ile Ser Ser Ser Ala Gly Ala
     515   520   525

Arg Trp Arg Glu Ala Leu Pro Gly Pro His Tyr Tyr Thr Trp Gly Asp
  530   535   540

His Gly Gly Ile Ile Met Ala Ile Ala Gln Gly Met Glu Thr Asn Glu
545   550   555   560

Leu Lys Tyr Ser Thr Asn Glu Gly Glu Thr Trp Lys Ala Phe Thr Phe
     565   570   575

Ser Glu Lys Pro Val Phe Val Tyr Gly Leu Leu Thr Glu Pro Gly Glu
                580   585   590

Lys Ser Thr Val Phe Thr Ile Phe Gly Ser Asn Lys Glu Asn Val His
         595   600   605

Ser Trp Leu Ile Leu Gln Val Asn Ala Thr Asp Ala Leu Gly Val Pro
     610   615   620

Cys Thr Glu Asn Asp Tyr Lys Leu Trp Ser Pro Ser Asp Glu Arg Gly
625   630   635   640

Asn Glu Cys Leu Leu Gly His Lys Thr Val Phe Lys Arg Arg Thr Pro
             645   650   655

His Ala Thr Cys Phe Asn Gly Glu Asp Phe Asp Arg Pro Val Val Val
         660   665   670

Ser Asn Cys Ser Cys Thr Arg Glu Asp Tyr Glu Cys Asp Phe Gly Phe
         675   680   685

Arg Met Ser Glu Asp Leu Ala Leu Glu Val Cys Val Pro Asp Pro Gly
     690   695   700

Phe Ser Gly Lys Ser Ser Pro Pro Val Pro Cys Pro Val Gly Ser Thr
705   710   715   720

Tyr Arg Arg Ser Arg Gly Tyr Arg Lys Ile Ser Gly Asp Thr Cys Ser
             725   730   735

Gly Gly Asp Val Glu Ala Arg Leu Glu Gly Glu Leu Val Pro Cys Pro
             740   745   750

Leu Ala Glu Glu Asn Glu Phe Ile Leu Tyr Ala Thr Arg Lys Ser Ile
         755   760   765

His Arg Tyr Asp Leu Ala Ser Gly Thr Thr Glu Gln Leu Pro Leu Thr
     770   775   780

Gly Leu Arg Ala Ala Val Ala Leu Asp Phe Asp Tyr Glu His Asn Cys
785   790   795   800

Leu Tyr Trp Ser Asp Leu Ala Leu Asp Val Ile Gln Arg Leu Cys Leu
                    805   810   815

Asn Gly Ser Thr Gly Gln Glu Val Ile Ile Asn Ser Asp Leu Glu Thr
                820   825   830

Val Glu Ala Leu Ala Phe Glu Pro Leu Ser Gln Leu Leu Tyr Trp Val
                835   840   845

Asp Ala Gly Phe Lys Lys Ile Glu Val Ala Asn Pro Asp Gly Asp Phe
        850   855   860

Arg Leu Thr Val Val Asn Ser Ser Val Leu Asp Arg Pro Arg Ala Leu
865   870   875   880

Val Leu Val Pro Gln Glu Gly Ile Met Phe Trp Thr Asp Trp Gly Asp
                885   890   895

Leu Lys Pro Gly Ile Tyr Arg Ser Asn Met Asp Gly Ser Ala Ala Tyr
            900   905   910

Arg Leu Val Ser Glu Asp Val Lys Trp Pro Asn Gly Ile Ser Val Asp
            915   920   925

Asp Gln Trp Ile Tyr Trp Thr Asp Ala Tyr Leu Asp Cys Ile Glu Arg
        930   935   940

Ile Thr Phe Ser Gly Gln Gln Arg Ser Val Ile Leu Asp Arg Leu Pro
945   950   955   960

His Pro Tyr Ala Ile Ala Val Phe Lys Asn Glu Ile Tyr Trp Asp Asp
                965   970   975

Trp Ser Gln Leu Ser Ile Phe Arg Ala Ser Lys Tyr Ser Gly Ser Gln
            980   985   990

Met Glu Ile Leu Ala Ser Gln Leu Thr Gly Leu Met Asp Met Lys Ile
            995   1000   1005

Phe Tyr Lys Gly Lys Asn Thr Gly Ser Asn Ala Cys Val Pro Arg Pro
    1010   1015   1020

Cys Ser Leu Leu Cys Leu Pro Arg Ala Asn Asn Ser Lys Ser Cys Arg
 1025   1030   1035   1040

Cys Pro Asp Gly Val Ala Ser Ser Val Leu Pro Ser Gly Asp Leu Met
      1045   1050   1055

Cys Asp Cys Pro Lys Gly Tyr Glu Leu Lys Asn Asn Thr Cys Val Lys
      1060   1065   1070

Glu Glu Asp Thr Cys Leu Arg Asn Gln Tyr Arg Cys Ser Asn Gly Asn
      1075   1080   1085

Cys Ile Asn Ser Ile Trp Trp Cys Asp Phe Asp Asn Asp Cys Gly Asp
    1090   1095   1100

Met Ser Asp Glu Lys Asn Cys Pro Thr Thr Ile Cys Asp Leu Asp Thr
 1105   1110   1115   1120

Gln Phe Arg Cys Gln Glu Ser Gly Thr Cys Ile Pro Leu Ser Tyr Lys
      1125   1130   1135

Cys Asp Leu Glu Asp Asp Cys Gly Asp Asn Ser Asp Glu Arg His Cys
        1140   1145   1150

Glu Met His Gln Cys Arg Ser Asp Glu Tyr Asn Cys Ser Ser Gly Met
      1155   1160   1165

Cys Ile Arg Ser Ser Trp Val Cys Asp Gly Asp Asn Asp Cys Arg Asp
    1170   1175   1180

Trp Ser Asp Glu Ala Asn Cys Thr Ala Ile Tyr His Thr Cys Glu Ala
 1185   1190   1195   1200

Ser Asn Phe Gln Cys Arg Asn Gly His Cys Ile Pro Gln Arg Trp Ala
        1205   1210   1215

Cys Asp Gly Asp Ala Asp Cys Gln Asp Gly Ser Asp Glu Asp Pro Ala
      1220   1225   1230

Asn Cys Glu Lys Lys Cys Asn Gly Phe Arg Cys Pro Asn Gly Thr Cys
    1235   1240   1245

Ile Pro Ser Thr Lys His Cys Asp Gly Leu His Asp Cys Ser Asp Gly
          1250   1255   1260

Ser Asp Glu Gln His Cys Glu Pro Leu Cys Thr Arg Phe Met Asp Phe
1265   1270   1275   1280

Val Cys Lys Asn Arg Gln Gln Cys Leu Phe His Ser Met Val Cys Asp
                1285   1290   1295

Gly Ile Ile Gln Cys Arg Asp Gly Ser Asp Glu Asp Pro Ala Phe Ala
                1300   1305   1310

Gly Cys Ser Arg Asp Pro Glu Phe His Lys Val Cys Asp Glu Phe Gly
          1315   1320   1325

Phe Gln Cys Gln Asn Gly Val Cys Ile Ser Leu Ile Trp Lys Cys Asp
          1330   1335   1340

Gly Met Asp Asp Cys Gly Asp Tyr Ser Asp Glu Ala Asn Cys Glu Asn
1345   1350   1355   1360

Pro Thr Glu Ala Pro Asn Cys Ser Arg Tyr Phe Gln Phe Arg Cys Asp
                1365   1370   1375

Asn Gly His Cys Ile Pro Asn Arg Trp Lys Cys Asp Arg Glu Asn Asp
                1380   1385   1390

Cys Gly Asp Trp Ser Asp Glu Lys Asp Cys Gly Asp Ser His Val Leu
          1395   1400   1405

Pro Ser Thr Thr Pro Ala Pro Ser Thr Cys Leu Pro Asn Tyr Tyr Arg
          1410   1415   1420

Cys Gly Gly Gly Ala Cys Val Ile Asp Thr Trp Val Cys Asp Gly Tyr
1425   1430   1435   1440

Arg Asp Cys Ala Asp Gly Ser Asp Glu Glu Ala Cys Pro Ser Leu Pro
                1445   1450   1455

Asn Val Thr Ala Thr Ser Ser Pro Ser Gln Pro Gly Arg Cys Asp Arg
          1460   1465   1470

Phe Glu Phe Glu Cys His Gln Pro Lys Lys Cys Ile Pro Asn Trp Arg
        1475   1480   1485

Arg Cys Asp Gly His Gln Asp Cys Gln Asp Gly Gln Asp Glu Ala Asn
        1490   1495   1500

Cys Pro Thr His Ser Thr Leu Thr Cys Met Ser Trp Glu Phe Lys Cys
1505   1510   1515   1520

Glu Asp Gly Glu Ala Cys Ile Val Leu Ser Glu Arg Cys Asp Gly Phe
                1525   1530   1535

Leu Asp Cys Ser Asp Glu Ser Asp Glu Lys Ala Cys Ser Asp Glu Leu
        1540   1545   1550

Thr Val Tyr Lys Val Gln Asn Leu Gln Trp Thr Ala Asp Phe Ser Gly
        1555   1560   1565

Asn Val Thr Leu Thr Trp Met Arg Pro Lys Lys Met Pro Ser Ala Ala
        1570   1575   1580

Cys Val Tyr Asn Val Tyr Tyr Arg Val Val Gly Glu Ser Ile Trp Lys
1585   1590   1595   1600

Thr Leu Glu Thr His Ser Asn Lys Thr Asn Thr Val Leu Lys Val Leu
                1605   1610   1615

Lys Pro Asp Thr Thr Tyr Gln Val Lys Val Gln Val Gln Cys Leu Ser
        1620   1625   1630

Lys Val His Asn Thr Asn Asp Phe Val Thr Leu Arg Thr Pro Glu Gly
        1635   1640   1645

Leu Pro Asp Ala Pro Gln Asn Leu Gln Leu Ser Leu His Gly Glu Glu
        1650   1655   1660

Glu Gly Val Ile Val Gly His Trp Ser Pro Pro Thr His Thr His Gly
1665   1670   1675   1680

Leu Ile Arg Glu Tyr Ile Val Glu Tyr Ser Arg Ser Gly Ser Lys Val
        1685   1690   1695

Trp Thr Ser Glu Arg Ala Ala Ser Asn Phe Thr Glu Ile Lys Asn Leu
     1700   1705   1710

Leu Val Asn Thr Leu Tyr Thr Val Arg Val Ala Ala Val Thr Ser Arg
    1715   1720   1725

Gly Ile Gly Asn Trp Ser Asp Ser Lys Ser Ile Thr Thr Val Lys Gly
    1730   1735   1740

Lys Ala Ile Pro Pro Pro Asn Ile His Ile Asp Asn Tyr Asp Glu Asn
1745   1750   1755   1760

Ser Leu Ser Phe Thr Leu Thr Val Asp Gly Asn Ile Lys Val Asn Gly
     1765   1770   1775

Tyr Val Val Asn Leu Phe Trp Ala Phe Asp Thr His Lys Gln Glu Lys
    1780   1785   1790

Lys Thr Met Asn Phe Gln Gly Ser Ser Val Ser His Lys Val Gly Asn
    1795   1800   1805

Leu Thr Ala Gln Thr Ala Tyr Glu Ile Ser Ala Trp Ala Lys Thr Asp
   1810   1815   1820

Leu Gly Asp Ser Pro Leu Ser Phe Glu His Val Thr Thr Arg Gly Val
1825   1830   1835   1840

Arg Pro Pro Ala Pro Ser Leu Lys Ala Arg Ala Ile Asn Gln Thr Ala
     1845   1850   1855

Val Glu Cys Thr Trp Thr Gly Pro Arg Asn Val Val Tyr Gly Ile Phe
     1860   1865   1870

Tyr Ala Thr Ser Phe Leu Asp Leu Tyr Arg Asn Pro Ser Ser Leu Thr
    1875   1880   1885

Thr Pro Leu His Asn Ala Thr Val Leu Val Gly Lys Asp Glu Gln Tyr
    1890   1895   1900

Leu Phe Leu Val Arg Val Val Met Pro Tyr Gln Gly Pro Ser Ser Asp
1905   1910   1915   1920

Tyr Val Val Val Lys Met Ile Pro Asp Ser Arg Leu Pro Pro Arg His
            1925   1930   1935

Leu His Ala Val His Thr Gly Lys Thr Ser Ala Val Ile Lys Trp Glu
        1940   1945   1950

Ser Pro Tyr Asp Ser Pro Asp Gln Asp Leu Phe Tyr Ala Ile Ala Val
        1955   1960   1965

Lys Asp Leu Ile Arg Lys Thr Asp Arg Ser Tyr Lys Val Lys Ser Arg
        1970   1975   1980

Asn Ser Thr Val Glu Tyr Thr Leu Ser Lys Leu Glu Pro Gly Gly Lys
1985   1990   1995   2000

Tyr His Val Ile Val Gln Leu Gly Asn Met Ser Lys Asp Ala Ser Val
        2005   2010   ·2015

Lys Ile Thr Thr Val Ser Leu Ser Ala Pro Asp Ala Leu Lys Ile Ile
        2020   2025   2030

Thr Glu Asn Asp His Val Leu Leu Phe Trp Lys Ser Leu Ala Leu Lys
        2035   2040   2045

Glu Lys Tyr Phe Asn Glu Ser Arg Gly Tyr Glu Ile His Met Phe Asp
        2050   2055   2060

Ser Ala Met Asn Ile Thr Ala Tyr Leu Gly Asn Thr Thr Asp Asn Phe
2065   2070   2075   2080

Phe Lys Ile Ser Asn Leu Lys Met Gly His Asn Tyr Thr Phe Thr Val
        2085   2090   2095

Gln Ala Arg Cys Leu Leu Gly Ser Gln Ile Cys Gly Glu Pro Ala Val
        2100   2105   2110

Leu Leu Tyr Asp Glu Leu Gly Ser Gly Gly Asp Ala Ser Ala Met Gln
        2115   2120   2125

Ala Ala Arg Ser Thr Asp Val Ala Ala Val Val Val Pro Ile Leu Phe
        2130   2135   2140

Leu Ile Leu Leu Ser Leu Gly Val Gly Phe Ala Ile Leu Tyr Thr Lys
   2145   2150   2155   2160

His Arg Arg Leu Gln Ser Ser Phe Thr Ala Phe Ala Asn Ser His Tyr
        2165   2170   2175

Ser Ser Arg Leu Gly Ser Ala Ile Phe Ser Ser Gly Asp Asp Leu Gly
        2180   2185   2190

Glu Asp Asp Glu Asp Ala Pro Met Ile Thr Gly Phe Ser Asp Asp Val
      2195   2200   2205

Pro Met Val Ile Ala
   2210

Sequence ID No. 3

Length of the Sequence: 6961

Type: nucleic acid

Strandedness: double

Topology: linear

Molecular type: cDNA to mRNA

Feature:

 Name/Key: sig peptide

 Location: 178..261

 Identification method: S

 Name/Key: mat peptide

 Location: 262..6816

 Identification method: S

Sequence:

CCGCGAGCCG CACACGTGAC GGCGCCGCGC CGCGCCGCGC CGCGCCGAGC GGGACCCAGC 60
GGCTGCCCGG AGCCCCGGGA GCGGCGCGCG CGCGGCCCCG GCCCCGCCGC TCGGCCGGCG 120
GCGCGCTGCA CATTCTCTCC TGGCGGCGGC GCCACCTGCA GCCGCGTTCG CCCGAACATG 180
                                                            Met

1

GCG ACA CGG AGC AGC AGG AGG GAG TCG CGA CTC CCC TTC CTA TTC ACC   228
Ala Thr Arg Ser Ser Arg Arg Glu Ser Arg Leu Pro Phe Leu Phe Thr
         5   10   15

CTG GTC GCG CTG CTG CCG CCC GGG GCT CTC TGC GAG GTG TGG ACG CGG   276
Leu Val Ala Leu Leu Pro Pro Gly Ala Leu Cys Glu Val Trp Thr Arg
         20   25   30

ACA CTG CAC GGC GGC CGC GCG CCC TTA CCC CAG GAG CGG GGC TTC CGC   324
Thr Leu His Gly Gly Arg Ala Pro Leu Pro Gln Glu Arg Gly Phe Arg
         35   40   45

GTG GTG CAG GGC GAC CCG CGC GAG CTG CGG CTG TGG GAG CGC GGG GAT   372
Val Val Gln Gly Asp Pro Arg Glu Leu Arg Leu Trp Glu Arg Gly Asp
50   55   60   65

GCC AGG GGG GCG AGC CGG GCG GAC GAG AAG CCG CTC CGG AGG AGA CGG   420
Ala Arg Gly Ala Ser Arg Ala Asp Glu Lys Pro Leu Arg Arg Arg Arg
             70   75   80

AGC GCT GCC CTG CAG CCC GAG CCC ATC AAG GTG TAC GGA CAG GTC AGC   468
Ser Ala Ala Leu Gln Pro Glu Pro Ile Lys Val Tyr Gly Gln Val Ser
             85   90   95

CTC AAT GAT TCC CAC AAT CAG ATG GTG GTG CAC TGG GCC GGA GAG AAA   516
Leu Asn Asp Ser His Asn Gln Met Val Val His Trp Ala Gly Glu Lys
           100   105   110

AGC AAC GTG ATC GTG GCC TTG GCC CGG GAC AGC CTG GCG TTG GCC AGG   564
Ser Asn Val Ile Val Ala Leu Ala Arg Asp Ser Leu Ala Leu Ala Arg
         115   120   125

CCC AGG AGC AGT GAT GTG TAC GTG TCT TAT GAC TAT GGA AAA TCA TTC   612
Pro Arg Ser Ser Asp Val Tyr Val Ser Tyr Asp Tyr Gly Lys Ser Phe
130   135   140   145

AAT AAG ATT TCA GAG AAA TTG AAC TTC GGC GCG GGA AAT AAC ACA GAG   660
Asn Lys Ile Ser Glu Lys Leu Asn Phe Gly Ala Gly Asn Asn Thr Glu
             150   155   160

GCT GTG GTG GCC CAG TTC TAC CAC AGC CCT GCG GAC AAC AAA CGG TAC   708
Ala Val Val Ala Gln Phe Tyr His Ser Pro Ala Asp Asn Lys Arg Tyr
             165   170   175

ATC TTC GCA GAT GCC TAC GCC CAG TAT CTC TGG ATC ACG TTT GAC TTC   756
Ile Phe Ala Asp Ala Tyr Ala Gln Tyr Leu Trp Ile Thr Phe Asp Phe
             180   185   190

TGC AAC ACC ATC CAT GGC TTT TCC ATC CCG TTC CGG GCA GCT GAT CTC   804
Cys Asn Thr Ile His Gly Phe Ser Ile Pro Phe Arg Ala Ala Asp Leu
             195   200   205

CTA CTC CAC AGT AAG GCC TCC AAC CTT CTC CTG GGC TTC GAC AGG TCT   852
Leu Leu His Ser Lys Ala Ser Asn Leu Leu Leu Gly Phe Asp Arg Ser
210   215   220   225

CAC CCC AAC AAG CAG CTG TGG AAG TCG GAT GAT TTT GGC CAG ACC TGG   900
His Pro Asn Lys Gln Leu Trp Lys Ser Asp Asp Phe Gly Gln Thr Trp
             230   235   240

ATC ATG ATT CAA GAA CAC GTG AAG TCC TTT TCT TGG GGA ATT GAT CCC   948
Ile Met Ile Gln Glu His Val Lys Ser Phe Ser Trp Gly Ile Asp Pro
             245   250   255

TAT GAC AAA CCA AAC ACC ATC TAC ATC GAA CGG CAC GAA CCT TCT GGC   996
Tyr Asp Lys Pro Asn Thr Ile Tyr Ile Glu Arg His Glu Pro Ser Gly
             260   265   270

TAC TCC ACG GTT TTC CGA AGT ACA GAC TTC TTC CAG TCC CGG GAA AAC   1044
Tyr Ser Thr Val Phe Arg Ser Thr Asp Phe Phe Gln Ser Arg Glu Asn
             275   280   285

CAG GAA GTG ATC TTG GAG GAA GTG AGA GAC TTT CAG CTT CGG GAC AAG   1092

23

Gln Glu Val Ile Leu Glu Glu Val Arg Asp Phe Gln Leu Arg Asp Lys
290   295   300   305

TAC ATG TTT GCT ACA AAG GTG GTG CAT CTC TTG GGC AGT CCA CTG CAG   1140
Tyr Met Phe Ala Thr Lys Val Val His Leu Leu Gly Ser Pro Leu Gln
                310   315   320

TCT TCT GTC CAG CTC TGG GTC TCC TTT GGC CGG AAG CCC ATG CGG GCC   1188
Ser Ser Val Gln Leu Trp Val Ser Phe Gly Arg Lys Pro Met Arg Ala
                325   330   335

GCC CAG TTT GTT ACA AGA CAT CCT ATC AAC GAA TAT TAC ATC GCG GAT   1236
Ala Gln Phe Val Thr Arg His Pro Ile Asn Glu Tyr Tyr Ile Ala Asp
            340   345   350

GCC TCG GAG GAC CAG GTG TTT GTG TGT GTC AGT CAC AGC AAC AAC CGC   1284
Ala Ser Glu Asp Gln Val Phe Val Cys Val Ser His Ser Asn Asn Arg
        355   360   365

ACC AAC CTC TAC ATC TCG GAG GCA GAG GGC TTG AAG TTC TCT CTG TCC   1332
Thr Asn Leu Tyr Ile Ser Glu Ala Glu Gly Leu Lys Phe Ser Leu Ser
370   375   380   385

CTG GAG AAC GTG CTC TAC TAC ACC CCG GGA GGG GCC GGC AGT GAC ACC   1380
Leu Glu Asn Val Leu Tyr Tyr Thr Pro Gly Gly Ala Gly Ser Asp Thr
                390   395   400

TTG GTG AGG TAC TTT GCA AAT GAA CCG TTT GCT GAC TTC CAT CGT GTG   1428
Leu Val Arg Tyr Phe Ala Asn Glu Pro Phe Ala Asp Phe His Arg Val
                405   410   415

GAA GGG TTG CAG GGA GTC TAC ATT GCT ACT CTG ATT AAT GGT TCT ATG   1476
Glu Gly Leu Gln Gly Val Tyr Ile Ala Thr Leu Ile Asn Gly Ser Met
            420   425   430

AAT GAG GAG AAC ATG AGA TCT GTC ATC ACC TTT GAC AAA GGG GGC ACC   1524
Asn Glu Glu Asn Met Arg Ser Val Ile Thr Phe Asp Lys Gly Gly Thr

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        435               440               445
TGG GAA TTT CTG CAG GCT CCA GCC TTC ACG GGG TAT GGA GAG AAA ATC   1572
Trp Glu Phe Leu Gln Ala Pro Ala Phe Thr Gly Tyr Gly Glu Lys Ile
450               455               460               465
AAC TGT GAG CTG TCC GAG GGC TGT TCC CTC CAC CTG GCC CAG CGC CTC   1620
Asn Cys Glu Leu Ser Glu Gly Cys Ser Leu His Leu Ala Gln Arg Leu
                  470               475               480
AGC CAG CTG CTC AAC CTC CAG CTC CGG AGG ATG CCC ATC CTG TCC AAG   1668
Ser Gln Leu Leu Asn Leu Gln Leu Arg Arg Met Pro Ile Leu Ser Lys
                  485               490               495
GAG TCG GCG CCT GGC CTC ATC ATT GCC ACG GGC TCA GTG GGA AAG AAC   1716
Glu Ser Ala Pro Gly Leu Ile Ile Ala Thr Gly Ser Val Gly Lys Asn
                  500               505               510
TTG GCT AGC AAG ACA AAC GTG TAC ATC TCT AGC AGT GCT GGA GCC AGG   1764
Leu Ala Ser Lys Thr Asn Val Tyr Ile Ser Ser Ser Ala Gly Ala Arg
                  515               520               525
TGG CGA GAG GCA CTT CCT GGA CCT CAC TAC TAT ACA TGG GGA GAC CAT   1812
Trp Arg Glu Ala Leu Pro Gly Pro His Tyr Tyr Thr Trp Gly Asp His
530               535               540               545
GGC GGC ATC ATC ATG GCC ATT GCC CAA GGC ATG GAA ACC AAC GAA CTG   1860
Gly Gly Ile Ile Met Ala Ile Ala Gln Gly Met Glu Thr Asn Glu Leu
                  550               555               560
AAG TAC AGT ACC AAC GAA GGG GAG ACC TGG AAA GCC TTC ACC TTC TCT   1908
Lys Tyr Ser Thr Asn Glu Gly Glu Thr Trp Lys Ala Phe Thr Phe Ser
                  565               570               575
GAG AAG CCC GTG TTT GTG TAT GGG CTC CTC ACG GAA CCC GGC GAG AAG   1956
Glu Lys Pro Val Phe Val Tyr Gly Leu Leu Thr Glu Pro Gly Glu Lys
                  580               585               590
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AGC ACG GTC TTC ACC ATC TTT GGC TCC AAC AAG GAG AAC GTG CAC AGC    2004
Ser Thr Val Phe Thr Ile Phe Gly Ser Asn Lys Glu Asn Val His Ser
    595                 600                 605

TGG CTC ATC CTC CAG GTC AAT GCC ACA GAC GCC CTG GGG GTT CCT TGC    2052
Trp Leu Ile Leu Gln Val Asn Ala Thr Asp Ala Leu Gly Val Pro Cys
610                 615                 620                 625

ACA GAG AAC GAC TAC AAG CTC TGG TCA CCA TCT GAT GAG CGG GGG AAT    2100
Thr Glu Asn Asp Tyr Lys Leu Trp Ser Pro Ser Asp Glu Arg Gly Asn
                630                 635                 640

GAG TGT TTG CTT GGA CAC AAG ACT GTT TTC AAA CGG AGG ACC CCG CAC    2148
Glu Cys Leu Leu Gly His Lys Thr Val Phe Lys Arg Arg Thr Pro His
                645                 650                 655

GCC ACA TGC TTT AAC GGA GAA GAC TTT GAC AGG CCG GTG GTT GTG TCC    2196
Ala Thr Cys Phe Asn Gly Glu Asp Phe Asp Arg Pro Val Val Val Ser
            660                 665                 670

AAC TGC TCC TGC ACC CGG GAG GAC TAT GAG TGT GAC TTT GGC TTC CGG    2244
Asn Cys Ser Cys Thr Arg Glu Asp Tyr Glu Cys Asp Phe Gly Phe Arg
            675                 680                 685

ATG AGT GAA GAC TTG GCA TTA GAG GTG TGT GTT CCA GAT CCA GGA TTT    2292
Met Ser Glu Asp Leu Ala Leu Glu Val Cys Val Pro Asp Pro Gly Phe
690                 695                 700                 705

TCT GGA AAG TCC TCC CCT CCA GTG CCT TGT CCC GTG GGC TCT ACG TAC    2340
Ser Gly Lys Ser Ser Pro Pro Val Pro Cys Pro Val Gly Ser Thr Tyr
                710                 715                 720

AGG CGA TCA AGA GGC TAC CGG AAG ATT TCT GGG GAC ACC TGT AGT GGA    2388
Arg Arg Ser Arg Gly Tyr Arg Lys Ile Ser Gly Asp Thr Cys Ser Gly
                725                 730                 735

GGA GAT GTT GAG GCA CGG CTA GAA GGA GAG CTG GTC CCC TGT CCC CTG    2436
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Gly Asp Val Glu Ala Arg Leu Glu Gly Glu Leu Val Pro Cys Pro Leu

       740   745   750

GCA GAA GAG AAC GAG TTC ATC CTG TAC GCC ACG CGC AAG TCC ATC CAC   2484

Ala Glu Glu Asn Glu Phe Ile Leu Tyr Ala Thr Arg Lys Ser Ile His

       755   760   765

CGC TAT GAC CTG GCT TCC GGA ACC ACG GAG CAG TTG CCC CTC ACT GGG   2532

Arg Tyr Asp Leu Ala Ser Gly Thr Thr Glu Gln Leu Pro Leu Thr Gly

770   775   780   785

TTC CGG GCA GCA GTG GCC CTG GAC TTT GAC TAT GAG CAC AAC TGC CTG   2580

Leu Arg Ala Ala Val Ala Leu Asp Phe Asp Tyr Glu His Asn Cys Leu

          790   795   800

TAT TGG TCT GAC CTG GCC TTG GAC GTC ATC CAG CGC CTC TGT TTG AAC   2628

Tyr Trp Ser Asp Leu Ala Leu Asp Val Ile Gln Arg Leu Cys Leu Asn

          805   810   815

GGG AGT ACA GGA CAA GAG GTG ATC ATC AAC TCT GAC CTG GAG ACG GTA   2676

Gly Ser Thr Gly Gln Glu Val Ile Ile Asn Ser Asp Leu Glu Thr Val

       820   825   830

GAA GCT TTG GCT TTT GAA CCC CTC AGC CAA TTA CTT TAC TGG GTG GAC   2724

Glu Ala Leu Ala Phe Glu Pro Leu Ser Gln Leu Leu Tyr Trp Val Asp

       835   840   845

GCA GGC TTT AAA AAG ATC GAG GTA GCC AAT CCA GAT GGT GAC TTC CGA   2772

Ala Gly Phe Lys Lys Ile Glu Val Ala Asn Pro Asp Gly Asp Phe Arg

850   855   860   865

CTC ACC GTC GTC AAT TCC TCG GTG CTG GAT CGG CCC CGG GCC CTG GTC   2820

Leu Thr Val Val Asn Ser Ser Val Leu Asp Arg Pro Arg Ala Leu Val

          870   875   880

CTT GTG CCC CAA GAA GGG ATC ATG TTC TGG ACC GAC TGG GGA GAC CTG   2868

Leu Val Pro Gln Glu Gly Ile Met Phe Trp Thr Asp Trp Gly Asp Leu

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              885                890                895
AAG CCT GGG ATT TAT CGG AGC AAC ATG GAC GGA TCT GCC GCC TAT CGC   2916
Lys Pro Gly Ile Tyr Arg Ser Asn Met Asp Gly Ser Ala Ala Tyr Arg
              900                905                910
CTC GTG TCG GAG GAT GTG AAG TGG CCC AAT GGC ATT TCC GTG GAC GAT   2964
Leu Val Ser Glu Asp Val Lys Trp Pro Asn Gly Ile Ser Val Asp Asp
          915                920                925
CAG TGG ATC TAC TGG ACG GAT GCC TAC CTG GAC TGC ATT GAG CGC ATC   3012
Gln Trp Ile Tyr Trp Thr Asp Ala Tyr Leu Asp Cys Ile Glu Arg Ile
930                935                940                945
ACG TTC AGC GGC CAG CAG CGC TCC GTC ATC CTG GAC AGA CTC CCG CAC   3060
Thr Phe Ser Gly Gln Gln Arg Ser Val Ile Leu Asp Arg Leu Pro His
              950                955                960
CCC TAT GCC ATT GCT GTC TTT AAG AAT GAG ATT TAC TGG GAT GAC TGG   3108
Pro Tyr Ala Ile Ala Val Phe Lys Asn Glu Ile Tyr Trp Asp Asp Trp
          965                970                975
TCA CAG CTC AGC ATA TTC CGA GCT TCT AAG TAC AGC GGG TCC CAG ATG   3156
Ser Gln Leu Ser Ile Phe Arg Ala Ser Lys Tyr Ser Gly Ser Gln Met
              980                985                990
GAG ATT CTG GCC AGC CAG CTC ACG GGG CTG ATG GAC ATG AAG ATC TTC   3204
Glu Ile Leu Ala Ser Gln Leu Thr Gly Leu Met Asp Met Lys Ile Phe
          995                1000               1005
TAC AAG GGG AAG AAC ACA GGA AGC AAT GCG TGT GTA CCC AGG CCG TGC   3252
Tyr Lys Gly Lys Asn Thr Gly Ser Asn Ala Cys Val Pro Arg Pro Cys
1010               1015               1020               1025
AGC CTG CTG TGC CTG CCC AGA GCC AAC AAC AGC AAA AGC TGC AGG TGT   3300
Ser Leu Leu Cys Leu Pro Arg Ala Asn Asn Ser Lys Ser Cys Arg Cys
          1030               1035               1040
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CCA GAT GGC GTG GCC AGC AGT GTC CTC CCT TCC GGG GAC CTG ATG TGT    3348
Pro Asp Gly Val Ala Ser Ser Val Leu Pro Ser Gly Asp Leu Met Cys
            1045             1050             1055

GAC TGC CCT AAG GGC TAC GAG CTG AAG AAC AAC ACG TGT GTC AAA GAA    3396
Asp Cys Pro Lys Gly Tyr Glu Leu Lys Asn Asn Thr Cys Val Lys Glu
            1060             1065             1070

GAA GAC ACC TGT CTG CGC AAC CAG TAC CGC TGC AGC AAC GGG AAC TGC    3444
Glu Asp Thr Cys Leu Arg Asn Gln Tyr Arg Cys Ser Asn Gly Asn Cys
            1075             1080             1085

ATC AAC AGC ATC TGG TGG TGC GAT TTC GAC AAC GAC TGC GGA GAC ATG    3492
Ile Asn Ser Ile Trp Trp Cys Asp Phe Asp Asn Asp Cys Gly Asp Met
1090             1095             1100             1105

AGC GAC GAG AAG AAC TGC CCT ACC ACC ATC TGC GAC CTG GAC ACC CAG    3540
Ser Asp Glu Lys Asn Cys Pro Thr Thr Ile Cys Asp Leu Asp Thr Gln
            1110             1115             1120

TTC CGT TGC CAG GAG TCT GGG ACG TGC ATC CCG CTC TCC TAC AAA TGT    3588
Phe Arg Cys Gln Glu Ser Gly Thr Cys Ile Pro Leu Ser Tyr Lys Cys
            1125             1130             1135

GAC CTC GAG GAT GAC TGT GGG GAC AAC AGT GAC GAA AGG CAC TGT GAA    3636
Asp Leu Glu Asp Asp Cys Gly Asp Asn Ser Asp Glu Arg His Cys Glu
            1140             1145             1150

ATG CAC CAG TGC CGG AGC GAC GAA TAC AAC TGC AGC TCG GGC ATG TGC    3684
Met His Gln Cys Arg Ser Asp Glu Tyr Asn Cys Ser Ser Gly Met Cys
            1155             1160             1165

ATC CGC TCC TCC TGG GTG TGC GAC GGG GAC AAC GAC TGC AGG GAC TGG    3732
Ile Arg Ser Ser Trp Val Cys Asp Gly Asp Asn Asp Cys Arg Asp Trp
1170             1175             1180             1185

TCC GAC GAG GCC AAC TGC ACA GCC ATC TAT CAC ACC TGT GAG GCC TCC    3780
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Ser Asp Glu Ala Asn Cys Thr Ala Ile Tyr His Thr Cys Glu Ala Ser
          1190   1195   1200

AAC TTC CAG TGC CGC AAC GGG CAC TGC ATC CCC CAG CGG TGG GCG TGT   3828
Asn Phe Gln Cys Arg Asn Gly His Cys Ile Pro Gln Arg Trp Ala Cys
            1205   1210   1215

GAC GGC GAC GCC GAC TGC CAG GAT GGC TCT GAT GAG GAT CCA GCC AAC   3876
Asp Gly Asp Ala Asp Cys Gln Asp Gly Ser Asp Glu Asp Pro Ala Asn
            1220   1225   1230

TGT GAG AAG AAG TGC AAC GGC TTC CGC TGC CCG AAC GGC ACC TGC ATT   3924
Cys Glu Lys Lys Cys Asn Gly Phe Arg Cys Pro Asn Gly Thr Cys Ile
        1235   1240   1245

CCC TCC ACC AAG CAC TGT GAC GGC CTG CAC GAT TGC TCG GAC GGC TCC   3972
Pro Ser Thr Lys His Cys Asp Gly Leu His Asp Cys Ser Asp Gly Ser
1250   1255   1260   1265

GAC GAG CAG CAC TGC GAG CCC CTG TGT ACA CGG TTC ATG GAC TTC GTG   4020
Asp Glu Gln His Cys Glu Pro Leu Cys Thr Arg Phe Met Asp Phe Val
            1270   1275   1280

TGT AAG AAC CGC CAG CAG TGC CTC TTC CAC TCC ATG GTG TGC GAT GGG   4068
Cys Lys Asn Arg Gln Gln Cys Leu Phe His Ser Met Val Cys Asp Gly
            1285   1290   1295

ATC ATC CAG TGC CGT GAC GGC TCC GAC GAG GAC CCA GCC TTT GCA GGA   4116
Ile Ile Gln Cys Arg Asp Gly Ser Asp Glu Asp Pro Ala Phe Ala Gly
            1300   1305   1310

TGC TCC CGA GAC CCC GAG TTC CAC AAG GTG TGC GAT GAG TTC GGC TTC   4164
Cys Ser Arg Asp Pro Glu Phe His Lys Val Cys Asp Glu Phe Gly Phe
            1315   1320   1325

CAG TGT CAG AAC GGC GTG TGC ATC AGC TTG ATC TGG AAG TGC GAC GGG   4212
Gln Cys Gln Asn Gly Val Cys Ile Ser Leu Ile Trp Lys Cys Asp Gly

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        1330            1335            1340            1345
     ATG GAT GAC TGC GGG GAC TAC TCC GAC GAG GCC AAC TGT GAA AAC CCC   4260
     Met Asp Asp Cys Gly Asp Tyr Ser Asp Glu Ala Asn Cys Glu Asn Pro        .

                     1350            1355            1360
     ACA GAA GCC CCC AAC TGC TCC CGC TAC TTC CAG TTC CGG TGT GAC AAT   4308
     Thr Glu Ala Pro Asn Cys Ser Arg Tyr Phe Gln Phe Arg Cys Asp Asn

                 1365            1370            1375
     GGC CAC TGC ATC CCC AAC AGG TGG AAG TGT GAC AGG GAG AAT GAC TGT   4356
     Gly His Cys Ile Pro Asn Arg Trp Lys Cys Asp Arg Glu Asn Asp Cys      .

                 1380            1385            1390
     GGG GAC TGG TCC GAC GAG AAG GAC TGT GGA GAT TCA CAT GTA CTT CCG   4404
     Gly Asp Trp Ser Asp Glu Lys Asp Cys Gly Asp Ser His Val Leu Pro

             1395            1400            1405
     TCT ACG ACT CCT GCA CCC TCC ACG TGT CTG CCC AAT TAC TAC CGC TGC   4452
     Ser Thr Thr Pro Ala Pro Ser Thr Cys Leu Pro Asn Tyr Tyr Arg Cys

     1410            1415            1420            1425
     GGC GGG GGG GCC TGC GTG ATA GAC ACG TGG GTT TGT GAC GGG TAC CGA   4500
     Gly Gly Gly Ala Cys Val Ile Asp Thr Trp Val Cys Asp Gly Tyr Arg

                     1430            1435          . 1440
     GAT TGC GCA GAT GGA TCC GAC GAG GAA GCC TGC CCC TCG CTC CCC AAT   4548
     Asp Cys Ala Asp Gly Ser Asp Glu Glu Ala Cys Pro Ser Leu Pro Asn

                 1445            1450            1455
     GTC ACT GCC ACC TCC TCC CCC TCC CAG CCT GGA CGA TGC GAC CGA TTT   4596
     Val Thr Ala Thr Ser Ser Pro Ser Gln Pro Gly Arg Cys Asp Arg Phe

             1460            1465            1470
     GAG TTT GAG TGC CAC CAG CCA AAG AAG TGC ATC CCT AAC TGG AGA CGC   4644
     Glu Phe Glu Cys His Gln Pro Lys Lys Cys Ile Pro Asn Trp Arg Arg

         1775            1480            1485
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TGT GAC GGC CAT CAG GAT TGC CAG GAT GGC CAG GAC GAG GCC AAC TGC   4692
Cys Asp Gly His Gln Asp Cys Gln Asp Gly Gln Asp Glu Ala Asn Cys
    1490   1495   1500   1505

CCC ACT CAC AGC ACC TTG ACC TGC ATG AGC TGG GAG TTC AAG TGT GAG   4740
Pro Thr His Ser Thr Leu Thr Cys Met Ser Trp Glu Phe Lys Cys Glu
        1510   1515   1520

GAT GGC GAG GCC TGC ATC GTG CTG TCA GAA CGC TGC GAC GGC TTC CTG   4788
Asp Gly Glu Ala Cys Ile Val Leu Ser Glu Arg Cys Asp Gly Phe Leu
      1525   1530   1535

GAC TGC TCA GAT GAG AGC GAC GAG AAG GCC TGC AGT GAT GAG TTA ACT   4836
Asp Cys Ser Asp Glu Ser Asp Glu Lys Ala Cys Ser Asp Glu Leu Thr
    1540   1545   1550

GTA TAC AAA GTA CAG AAT CTT CAG TGG ACA GCT GAC TTC TCT GGG AAT   4884
Val Tyr Lys Val Gln Asn Leu Gln Trp Thr Ala Asp Phe Ser Gly Asn
   1555   1560   1565

GTC ACT TTG ACC TGG ATG CGG CCC AAA AAA ATG CCC TCT GCT GCT TGT   4932
Val Thr Leu Thr Trp Met Arg Pro Lys Lys Met Pro Ser Ala Ala Cys
1570   1575   1580   1585

GTA TAC AAC GTG TAC TAT AGA GTT GTT GGA GAG AGC ATA TGG AAG ACT   4980
Val Tyr Asn Val Tyr Tyr Arg Val Val Gly Glu Ser Ile Trp Lys Thr
     1590   1595   1600

CTG GAG ACT CAC AGC AAT AAG ACA AAC ACT GTA TTA AAA GTG TTG AAA   5028
Leu Glu Thr His Ser Asn Lys Thr Asn Thr Val Leu Lys Val Leu Lys
      1605   1610   1615

CCA GAT ACC ACC TAC CAG GTT AAA GTG CAG GTT CAG TGC CTG AGC AAG   5076
Pro Asp Thr Thr Tyr Gln Val Lys Val Gln Val Gln Cys Leu Ser Lys
     1620   1625   1630

GTG CAC AAC ACC AAT GAC TTT GTG ACC TTG AGA ACT CCA GAG GGA TTG   5124

Val His Asn Thr Asn Asp Phe Val Thr Leu Arg Thr Pro Glu Gly Leu

    1635   1640   1645

CCA GAC GCC CCT CAG AAC CTC CAG CTG TCG CTC CAC GGG GAA GAG GAA   5172

Pro Asp Ala Pro Gln Asn Leu Gln Leu Ser Leu His Gly Glu Glu Glu

1650   1655   1660   1665

GGT GTG ATT GTG GGC CAC TGG AGC CCT CCC ACC CAC ACC CAC GGC CTC   5220

Gly Val Ile Val Gly His Trp Ser Pro Pro Thr His Thr His Gly Leu

        1670   1675   1680

ATT CGC GAA TAC ATT GTA GAG TAT AGC AGG AGT GGT TCC AAG GTG TGG   5268

Ile Arg Glu Tyr Ile Val Glu Tyr Ser Arg Ser Gly Ser Lys Val Trp

        1685   1690   1695

ACT TCA GAA AGG GCT GCT AGT AAC TTT ACA GAA ATA AAG AAC TTG TTG   5316

Thr Ser Glu Arg Ala Ala Ser Asn Phe Thr Glu Ile Lys Asn Leu Leu

    1700   1705   1710

GTC AAC ACC CTG TAC ACC GTC AGA GTG GCT GCG GTG ACG AGT CGT GGG   5364

Val Asn Thr Leu Tyr Thr Val Arg Val Ala Ala Val Thr Ser Arg Gly

    1715   1720   1725

ATA GGA AAC TGG AGC GAT TCC AAA TCC ATT ACC ACC GTG AAA GGA AAA   5412

Ile Gly Asn Trp Ser Asp Ser Lys Ser Ile Thr Thr Val Lys Gly Lys

1730   1735   1740   1745

GCG ATC CCG CCA CCA AAT ATC CAC ATT GAC AAC TAC GAT GAA AAT TCC   5460

Ala Ile Pro Pro Pro Asn Ile His Ile Asp Asn Tyr Asp Glu Asn Ser

        1750   1755   1760

CTG AGT TTT ACC CTG ACC GTG GAT GGG AAC ATC AAG GTG AAT GGC TAT   5508

Leu Ser Phe Thr Leu Thr Val Asp Gly Asn Ile Lys Val Asn Gly Tyr

        1765   1770   1775

GTG GTG AAC CTT TTC TGG GCA TTT GAC ACC CAC AAA CAA GAG AAG AAA   5556

Val Val Asn Leu Phe Trp Ala Phe Asp Thr His Lys Gln Glu Lys Lys

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                1780                    1785                    1790
 5    ACC ATG AAC TTC CAA GGG AGC TCA GTG TCC CAC AAA GTT GGC AAT CTG    5604
      Thr Met Asn Phe Gln Gly Ser Ser Val Ser His Lys Val Gly Asn Leu
          1795                    1800                    1805
10    ACA GCA CAG ACG GCC TAT GAG ATT TCC GCC TGG GCC AAG ACT GAC TTG    5652
      Thr Ala Gln Thr Ala Tyr Glu Ile Ser Ala Trp Ala Lys Thr Asp Leu
      1810                    1815                    1820                1825
15    GGC GAT AGT CCT CTG TCA TTT GAG CAT GTC ACG ACC AGA GGG GTT CGC    5700
      Gly Asp Ser Pro Leu Ser Phe Glu His Val Thr Thr Arg Gly Val Arg
                        1830                    1835                1840
20    CCA CCT GCT CCT AGC CTC AAG GCC AGG GCT ATC AAT CAG ACT GCA GTG    5748
      Pro Pro Ala Pro Ser Leu Lys Ala Arg Ala Ile Asn Gln Thr Ala Val
                    1845                    1850                    1855
25    GAA TGC ACC TGG ACA GGC CCC AGG AAT GTG GTG TAT GGC ATT TTC TAT    5796
      Glu Cys Thr Trp Thr Gly Pro Arg Asn Val Val Tyr Gly Ile Phe Tyr
                1860                    1865                    1870
30    GCC ACA TCC TTC CTG GAC CTC TAC CGC AAC CCA AGC AGC CTG ACC ACG    5844
      Ala Thr Ser Phe Leu Asp Leu Tyr Arg Asn Pro Ser Ser Leu Thr Thr
                1875                    1880                    1885
35    CCG CTG CAC AAC GCA ACC GTG CTC GTC GGT AAG GAT GAG CAG TAT CTG    5892
      Pro Leu His Asn Ala Thr Val Leu Val Gly Lys Asp Glu Gln Tyr Leu
      1890                    1895                    1900                1905
40    TTT CTG GTC CGG GTG GTG ATG CCC TAC CAA GGG CCG TCC TCG GAC TAC    5940
      Phe Leu Val Arg Val Val Met Pro Tyr Gln Gly Pro Ser Ser Asp Tyr
                    1910                    1915                    1920
45    GTG GTC GTG AAG ATG ATC CCG GAC AGC AGG CTT CCT CCC CGG CAC CTG    5988
      Val Val Val Lys Met Ile Pro Asp Ser Arg Leu Pro Pro Arg His Leu
                    1925                    1930                    1935
50
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CAT GCC GTT CAC ACC GGC AAG ACC TCG GCC GTC ATC AAG TGG GAG TCG   6036
His Ala Val His Thr Gly Lys Thr Ser Ala Val Ile Lys Trp Glu Ser
        1940   1945   1950

CCC TAC GAC TCT CCT GAC CAG GAC CTG TTC TAT GCG ATC GCA GTT AAA   6084
Pro Tyr Asp Ser Pro Asp Gln Asp Leu Phe Tyr Ala Ile Ala Val Lys
        1955   1960   1965

GAT CTG ATA CGA AAG ACG GAC CGG AGC TAC AAA GTC AAG TCC CGC AAC   6132
Asp Leu Ile Arg Lys Thr Asp Arg Ser Tyr Lys Val Lys Ser Arg Asn
1970   1975   1980   1985

AGC ACC GTG GAG TAC ACC CTG AGC AAG CTG GAG CCC GGA GGG AAA TAC   6180
Ser Thr Val Glu Tyr Thr Leu Ser Lys Leu Glu Pro Gly Gly Lys Tyr
        1990   1995   2000

CAC GTC ATT GTG CAG CTG GGG AAC ATG AGC AAA GAT GCC AGT GTG AAG   6228
His Val Ile Val Gln Leu Gly Asn Met Ser Lys Asp Ala Ser Val Lys
        2005   2010   2015

ATC ACC ACC GTT TCG TTA TCG GCA CCC GAT GCC TTA AAA ATC ATA ACA   6276
Ile Thr Thr Val Ser Leu Ser Ala Pro Asp Ala Leu Lys Ile Ile Thr
        2020   2025   2030

GAA AAT GAC CAC GTC CTT CTC TTC TGG AAA AGT CTA GCT CTA AAG GAA   6324
Glu Asn Asp His Val Leu Leu Phe Trp Lys Ser Leu Ala Leu Lys Glu
        2035   2040   2045

AAG TAT TTT AAC GAA AGC AGG GGC TAC GAG ATA CAC ATG TTT GAT AGC   6372
Lys Tyr Phe Asn Glu Ser Arg Gly Tyr Glu Ile His Met Phe Asp Ser
2050   2055   2060   2065

GCC ATG AAT ATC ACC GCA TAC CTT GGG AAT ACT ACT GAC AAT TTC TTT   6420
Ala Met Asn Ile Thr Ala Tyr Leu Gly Asn Thr Thr Asp Asn Phe Phe
        2070   2075   2080

AAA ATT TCC AAC CTG AAG ATG GGT CAC AAT TAC ACA TTC ACG GTC CAG   6468

Lys Ile Ser Asn Leu Lys Met Gly His Asn Tyr Thr Phe Thr Val Gln
          2085   2090   2095

GCA CGA TGC CTT TTG GGC AGC CAG ATC TGC GGG GAG CCT GCC GTG CTA   6516
Ala Arg Cys Leu Leu Gly Ser Gln Ile Cys Gly Glu Pro Ala Val Leu
          2100   2105   2110

CTG TAT GAT GAG CTG GGG TCT GGT GGC GAT GCG TCG GCG ATG CAG GCT   6564
Leu Tyr Asp Glu Leu Gly Ser Gly Gly Asp Ala Ser Ala Met Gln Ala
        2115   2120   2125

GCC AGG TCT ACT GAT GTC GCC GCC GTG GTG GTG CCC ATC CTG TTT CTG   6612
Ala Arg Ser Thr Asp Val Ala Ala Val Val Val Pro Ile Leu Phe Leu
2130   2135   2140   2145

ATA CTG CTG AGC CTG GGG GTC GGG TTT GCC ATC CTG TAC ACG AAG CAT   6660
Ile Leu Leu Ser Leu Gly Val Gly Phe Ala Ile Leu Tyr Thr Lys His
          2150   2155   2160

CGG AGG CTG CAG AGC AGC TTC ACC GCC TTC GCC AAC AGC CAC TAC AGC   6708
Arg Arg Leu Gln Ser Ser Phe Thr Ala Phe Ala Asn Ser His Tyr Ser
          2165   2170   2175

TCC AGA CTC GGC TCC GCC ATC TTC TCC TCT GGG GAT GAC TTG GGG GAG   6756
Ser Arg Leu Gly Ser Ala Ile Phe Ser Ser Gly Asp Asp Leu Gly Glu
        2180   2185   2190

GAT GAT GAA GAT GCT CCT ATG ATC ACT GGA TTT TCG GAC GAC GTC CCC   6804
Asp Asp Glu Asp Ala Pro Met Ile Thr Gly Phe Ser Asp Asp Val Pro
        2195   2200   2205

ATG GTG ATA GCC TGAAAGAGCT TTCCTCACTA GAAACCAAAT GGTGTAAATA   6856
Met Val Ile Ala
2210

TTTTATTTGA TAAAGATAGT TGATGGTTTA TTTTAAAAGA TGCACTTTGA GTTGCAATAT 6916
GTTATTTTTA TATGGGCCAA AAACAAAAGC AAAAAAAAAA AAAAA   6961

Sequence ID No. 4

Length of the Sequence: 300

Type: nucleic acid

Strandedness: double

Topology: linear

Molecular type: cDNA to mRNA

Sequence:

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ATATCCACAT TGACAGCTAT GGTGAAAATT ATCTAAGCTT CACCCTGACC ATGGAGAGTG   60

ATATCAAGGT GAATGGCTAT GTGGTGAACC TTTTCTGGGC ATTTGACACC CACAAGCAAG  120

AGAGGAGAAC TTTGAACTTC CGAGGAAGCA TATTGTCACA CAAAGTTGGC AATCTGACAG  180

CTCATACATC CTATGAGATT TCTGCCTGGG CCAAGACTGA CTTGGGGGAT AGCCCTCTGG  240

CATTTGAGCA TGTTATGACC AGAGGGGTTC GCCCACCTGC ACCTAGCCTC AAGGCCAAAG  300
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Sequence ID No. 5

Length of the Sequence: 6642

Type: nucleic acid

Strandedness: double

Topology: linear

Molecular type: cDNA to mRNA

Sequence:

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ATGGCGACAC GGAGCAGCAG GAGGGAGTCG CGACTCCCGT TCCTATTCAC CCTGGTCGCA   60

CTGCTGCCGC CCGGAGCTCT CTGCGAAGTC TGGACGCAGA GGCTGCACGG CGGCAGCGCG  120

CCCTTGCCCC AGGACCGGGG CTTCCTCGTG GTGCAGGGCG ACCCGCGCGA GCTGCGGCTG  180

TGGGCGCGCG GGGATGCCAG GGGGGCGAGC CGCGCGGACG AGAAGCCGCT CCGGAGGAAA  240

CGGAGCGCTG CCCTGCAGCC CGAGCCCATC AAGGTGTACG GACAGGTTAG TCTGAATGAT  300

TCCCACAATC AGATGGTGGT GCACTGGGCT GGAGAGAAAA GCAACGTGAT CGTGGCCTTG  360

GCCCGAGATA GCCTGGCATT GGCGAGGCCC AAGAGCAGTG ATGTGTACGT GTCTTACGAC  420

TATGGAAAAT CATTCAAGAA AATTTCAGAC AAGTTAAACT TTGGCTTGGG AAATAGGAGT  480
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GAAGCTGTTA TCGCCCAGTT CTACCACAGC CCTGCGGACA ACAAGCGGTA CATCTTTGCA    540

GACGCTTATG CCCAGTACCT CTGGATCACG TTTGACTTCT GCAACACTCT TCAAGGCTTT    600

TCCATCCCAT TTCGGGCAGC TGATCTCCTC CTACACAGTA AGGCCTCCAA CCTTCTCTTG    660

GGCTTTGACA GGTCCCACCC CAACAAGCAG CTGTGGAAGT CAGATGACTT TGGCCAGACC    720

TGGATCATGA TTCAGGAACA TGTCAAGTCC TTTTCTTGGG GAATTGATCC CTATGACAAA    780

CCAAATACCA TCTACATTGA ACGACACGAA CCCTCTGGCT ACTCCACTGT CTTCCGAAGT    840

ACAGATTTCT TCCAGTCCCG GGAAAACCAG GAAGTGATCC TTGAGGAAGT GAGAGATTTT    900

CAGCTTCGGG ACAAGTACAT GTTTGCTACA AAGGTGGTGC ATCTCTTGGG CAGTGAACAG    960

CAGTCTTCTG TCCAGCTCTG GGTCTCCTTT GGCCGGAAGC CCATGAGAGC AGCCCAGTTT   1020

GTCACAAGAC ATCCTATTAA TGAATATTAC ATCGCAGATG CCTCCGAGGA CCAGGTGTTT   1080

GTGTGTGTCA GCCACAGTAA CAACCGCACC AATTTATACA TCTCAGAGGC AGAGGGGCTG   1140

AAGTTCTCCC TGTCCTTGGA GAACGTGCTC TATTACAGCC CAGGAGGGGC CGGCAGTGAC   1200

ACCTTGGTGA GGTATTTTGC AAATGAACCA TTTGCTGACT TCCACCGAGT GGAAGGATTG   1260

CAAGGAGTCT ACATTGCTAC TCTGATTAAT GGTTCTATGA ATGAGGAGAA CATGAGATCG   1320

GTCATCACCT TTGACAAAGG GGGAACCTGG GAGTTTCTTC AGGCTCCAGC CTTCACGGGA   1380

TATGGAGAGA AAATCAATTG TGAGCTTTCC CAGGGCTGTT CCCTTCATCT GGCTCAGCGC   1440

CTCAGTCAGC TCCTCAACCT CCAGCTCCGG AGAATGCCCA TCCTGTCCAA GGAGTCGGCT   1500

CCAGGCCTCA TCATCGCCAC TGGCTCAGTG GGAAAGAACT TGGCTAGCAA GACAAACGTG   1560

TACATCTCTA GCAGTGCTGG AGCCAGGTGG CGAGAGGCAC TTCCTGGACC TCACTACTAC   1620

ACATGGGGAG ACCACGGCGG AATCATCACG GCCATTGCCC AGGGCATGGA AACCAACGAG   1680

CTAAAATACA GTACCAATGA AGGGGAGACC TGGAAAACAT TCATCTTCTC TGAGAAGCCA   1740

GTGTTTGTGT ATGGCCTCCT CACAGAACCT GGGGAGAAGA GCACTGTCTT CACCATCTTT   1800

GGCTCGAACA AAGAGAATGT CCACAGCTGG CTGATCCTCC AGGTCAATGC CACGGATGCC   1860

TTGGGAGTTC CCTGCACAGA GAATGACTAC AAGCTGTGGT CACCATCTGA TGAGCGGGGG   1920

AATGAGTGTT TGCTGGGACA CAAGACTGTT TTCAAACGGC GGACCCCCCA TGCCACATGC   1980

TTCAATGGAG AGGACTTTGA CAGGCCGGTG GTCGTGTCCA ACTGCTCCTG CACCCGGGAG   2040

GACTATGAGT GTGACTTCGG TTTCAAGATG AGTGAAGATT TGTCATTAGA GGTTTGTGTT   2100

CCAGATCCGG AATTTTCTGG AAAGTCATAC TCCCCTCCTG TGCCTTGCCC TGTGGGTTCT   2160
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38

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ACTTACAGGA GAACGAGAGG CTACCGGAAG ATTTCTGGGG ACACTTGTAG CGGAGGAGAT 2220

GTTGAAGCGC GACTGGAAGG AGAGCTGGTC CCCTGTCCCC TGGCAGAAGA GAACGAGTTC 2280

ATTCTGTATG CTGTGAGGAA ATCCATCTAC CGCTATGACC TGGCCTCGGG AGCCACCGAG 2340

CAGTTGCCTC TCACCGGGCT ACGGGCAGCA GTGGCCCTGG ACTTTGACTA TGAGCACAAC · 2400

TGTTTGTATT GGTCCGACCT GGCCTTGGAC GTCATCCAGC GCCTCTGTTT GAATGGAAGC 2460

ACAGGGCAAG AGGTGATCAT CAATTCTGGC CTGGAGACAG TAGAAGCTTT GGCTTTTGAA 2520

CCCCTCAGCC AGCTGCTTTA CTGGGTAGAT GCAGGCTTCA AAAAGATTGA GGTAGCTAAT 2580

CCAGATGGCG ACTTCCGACT CACAATCGTC AATTCCTCTG TGCTTGATCG TCCCAGGGCT 2640

CTGGTCCTCG TGCCCCAAGA GGGGGTGATG TTCTGGACAG ACTGGGGAGA CCTGAAGCCT 2700

GGGATTTATC GGAGCAATAT GGATGGTTCT GCTGCCTATC ACCTGGTGTC TGAGGATGTG 2760

AAGTGGCCCA ATGGCATCTC TGTGGACGAC CAGTGGATTT ACTGGACGGA TGCCTACCTG 2820

GAGTGCATAG AGCGGATCAC GTTCAGTGGC CAGCAGCGCT CTGTCATTCT GGACAACCTC 2880

CCGCACCCCT ATGCCATTGC TGTCTTTAAG AATGAAATCT ACTGGGATGA CTGGTCACAG 2940

CTCAGCATAT TCCGAGCTTC CAAATACAGT GGGTCCCAGA TGGAGATTCT GGCAAACCAG 3000

CTCACGGGGC TCATGGACAT GAAGATTTTC TACAAGGGGA AGAACACTGG AAGCAATGCC 3060

TGTGTGCCCA GGCCATGCAG CCTGCTGTGC CTGCCCAAGG CCAACAACAG TAGAAGCTGC 3120

AGGTGTCCAG AGGATGTGTC CAGCAGTGTG CTTCCATCAG GGGACCTGAT GTGTGACTGC 3180

CCTCAGGGCT ATCAGCTCAA GAACAATACC TGTGTCAAAG AAGAGAACAC CTGTCTTCGC 3240

AACCAGTATC GCTGCAGCAA CGGGAACTGT ATCAACAGCA TTTGGTGGTG TGACTTTGAC 3300

AACGACTGTG GAGACATGAG CGATGAGAGA AACTGCCCTA CCACCATCTG TGACCTGGAC 3360

ACCCAGTTTC GTTGCCAGGA GTCTGGGACT TGTATCCCAC TGTCCTATAA ATGTGACCTT 3420

GAGGATGACT GTGGAGACAA CAGTGATGAA AGTCATTGTG AAATGCACCA GTGCCGGAGT 3480

GACGAGTACA ACTGCAGTTC CGGCATGTGC ATCCGCTCCT CCTGGGTATG TGACGGGGAC 3540

AACGACTGCA GGGACTGGTC TGATGAAGCC AACTGTACCG CCATCTATCA CACCTGTGAG 3600

GCCTCCAACT TCCAGTGCCG AAACGGGCAC TGCATCCCCC AGCGGTGGGC GTGTGACGGG 3660

GATACGGACT GCCAGGATGG TTCCGATGAG GATCCAGTCA ACTGTGAGAA GAAGTGCAAT 3720

GGATTCCGCT GCCCAAACGG CACTTGCATC CCATCCAGCA AACATTGTGA TGGTCTGCGT 3780

GATTGCTCTG ATGGCTCCGA TGAACAGCAC TGCGAGCCCC TCTGTACGCA CTTCATGGAC 3840
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TTTGTGTGTA AGAACCGCCA GCAGTGCCTG TTCCACTCCA TGGTCTGTGA CGGAATCATC   3900

CAGTGCCGCG ACGGGTCCGA TGAGGATGCG GCGTTTGCAG GATGCTCCCA AGATCCTGAG   3960

TTCCACAAGG TATGTGATGA GTTCGGTTTC CAGTGTCAGA ATGGAGTGTG CATCAGTTTG   4020

ATTTGGAAGT GCGACGGGAT GGATGATTGC GGCGATTATT CTGATGAAGC CAACTGCGAA   4080

AACCCCACAG AAGCCCCAAA CTGCTCCCGC TACTTCCAGT TTCGGTGTGA GAATGGCCAC · 4140

TGCATCCCCA ACAGATGGAA ATGTGACAGG GAGAACGACT GTGGGGACTG GTCTGATGAG   4200

AAGGATTGTG GAGATTCACA TATTCTTCCC TTCTCGACTC CTGGGCCCTC CACGTGTCTG   4260

CCCAATTACT ACCGCTGCAG CAGTGGGACC TGCGTGATGG ACACCTGGCT GTGCGACGGG   4320

TACCGAGATT GTGCAGATGG CTCTGACGAG GAAGCCTGCC CCTTGCTTGC AAACGTCACT   4380

GCTGCCTCCA CTCCCACCCA ACTTGGGCGA TGTGACCGAT TTGAGTTCGA ATGCCACCAA   4440

CCGAAGACGT GTATTCCCAA CTGGAAGCGC TGTGACGGCC ACCAAGATTG CCAGGATGGC   4500

CGGGACGAGG CCAATTGCCC CACACACAGC ACCTTGACTT GCATGAGCAG GGAGTTCCAG   4560

TGCGAGGACG GGGAGGCCTG CATTGTGCTC TCGGAGCGCT GCGACGGCTT CCTGGACTGC   4620

TCGGACGAGA GCGATGAAAA GGCCTGCAGT GATGAGTTGA CTGTGTACAA AGTACAGAAT   4680

CTTCAGTGGA CAGCTGACTT CTCTGGGGAT GTGACTTTGA CCTGGATGAG GCCCAAAAAA   4740

ATGCCCTCTG CATCTTGTGT ATATAATGTC TACTACAGGG TGGTTGGAGA GAGCATATGG   4800

AAGACTCTGG AGACCCACAG CAATAAGACA AACACTGTAT TAAAAGTCTT GAAACCAGAT   4860

ACCACGTATC AGGTTAAAGT ACAGGTTCAG TGTCTCAGCA AGGCACACAA CACCAATGAC   4920

TTTGTGACCC TGAGGACCCC AGAGGGATTG CCAGATGCCC CTCGAAATCT CCAGCTGTCA   4980

CTCCCCAGGG AAGCAGAAGG TGTGATTGTA GGCCACTGGG CTCCTCCCAT CCACACCCAT   5040

GGCCTCATCC GTGAGTACAT TGTAGAATAC AGCAGGAGTG GTTCCAAGAT GTGGGCCTCC   5100

CAGAGGGCTG CTAGTAACTT TACAGAAATC AAGAACTTAT TGGTCAACAC TCTATACACC   5160

GTCAGAGTGG CTGCGGTGAC TAGTCGTGGA ATAGGAAACT GGAGCGATTC TAAATCCATT   5220

ACCACCATAA AAGGAAAAGT GATCCCACCA CCAGATATCC ACATTGACAG CTATGGTGAA   5280

AATTATCTAA GCTTCACCCT GACCATGGAG AGTGATATCA AGGTGAATGG CTATGTGGTG   5340

AACCTTTTCT GGGCATTTGA CACCCACAAG CAAGAGAGGA GAACTTTGAA CTTCCGAGGA   5400

AGCATATTGT CACACAAAGT TGGCAATCTG ACAGCTCATA CATCCTATGA GATTTCTGCC   5460

TGGGCCAAGA CTGACTTGGG GGATAGCCCT CTGGCATTTG AGCATGTTAT GACCAGAGGG   5520
```

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GTTCGCCCAC CTGCACCTAG CCTCAAGGCC AAAGCCATCA ACCAGACTGC AGTGGAATGT    5580

ACCTGGACCG GCCCCCGGAA TGTGGTTTAT GGTATTTTCT ATGCCACGTC CTTTCTTGAC    5640

CTCTATCGCA ACCCGAAGAG CTTGACTACT TCACTCCACA ACAAGACGGT CATTGTCAGT    5700

AAGGATGAGC AGTATTTGTT TCTGGTCCGT GTAGTGGTAC CCTACCAGGG GCCATCCTCT    5760

GACTACGTTG TAGTGAAGAT GATCCCGGAC AGCAGGCTTC CACCCCGTCA CCTGCATGTG    5820

GTTCATACGG GCAAAACCTC CGTGGTCATC AAGTGGGAAT CACCGTATGA CTCTCCTGAC    5880

CAGGACTTGT TGTATGCAAT TGCAGTCAAA GATCTCATAA GAAAGACTGA CAGGAGCTAC    5940

AAAGTAAAAT CCCGTAACAG CACTGTGGAA TACACCCTTA ACAAGTTGGA GCCTGGCGGG    6000

AAATACCACA TCATTGTCCA ACTGGGGAAC ATGAGCAAAG ATTCCAGCAT AAAAATTACC    6060

ACAGTTTCAT TATCAGCACC TGATGCCTTA AAAATCATAA CAGAAAATGA TCATGTTCTT    6120

CTCTTTTGGA AAAGCCTGGC TTTAAAGGAA AAGCATTTTA ATGAAAGCAG GGGCTATGAG    6180

ATACACATGT TTGATAGTGC CATGAATATC ACAGCTTACC TTGGGAATAC TACTGACAAT    6240

TTCTTTAAAA TTTCCAACCT GAAGATGGGT CATAATTACA CGTTCACCGT CCAAGCAAGA    6300

TGCCTTTTTG GCAACCAGAT CTGTGGGGAG CCTGCCATCC TGCTGTACGA TGAGCTGGGG    6360

TCTCGTGCAG ATGCATCTGC AACGCAGGCT GCCAGATCTA CGGATGTTGC TGCTGTGGTG    6420

GTGCCCATCT TATTCCTGAT ACTGCTGAGC CTGGGGGTGG GGTTTGCCAT CCTGTACACG    6480

AAGCACCGGA GGCTGCAGAG CAGCTTCACC GCCTTCGCCA ACAGCCACTA CAGCTCCAGG    6540

CTGGGGTCCG CAATCTTCTC CTCTGGGGAT GACCTGGGGG AAGATGATGA AGATGCCCCT    6600

ATGATAACTG GATTTTCAGA TGACGTCCCC ATGGTGATAG CC                      6642
```

Sequence ID No. 6

Length of the Sequence: 2214

Type: amino acid

Topology: linear

Molecular type: Protein

Sequence:

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Met Ala Thr Arg Ser Ser Arg Arg Glu Ser Arg Leu Pro Phe Leu Phe
                  5                  10                  15

Thr Leu Val Ala Leu Leu Pro Pro Gly Ala Leu Cys Glu Val Trp Thr
```

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                    20                    25                    30
     Gln Arg Leu His Gly Gly Ser Ala Pro Leu Pro Gln Asp Arg Gly Phe
                    35                    40                    45
     Leu Val Val Gln Gly Asp Pro Arg Glu Leu Arg Leu Trp Ala Arg Gly
                    50                    55                    60
     Asp Ala Arg Gly Ala Ser Arg Ala Asp Glu Lys Pro Leu Arg Arg Lys
                 65                    70                    75                    80
     Arg Ser Ala Ala Leu Gln Pro Glu Pro Ile Lys Val Tyr Gly Gln Val
                          85                    90                    95
     Ser Leu Asn Asp Ser His Asn Gln Met Val Val His Trp Ala Gly Glu
                         100                   105                   110
     Lys Ser Asn Val Ile Val Ala Leu Ala Arg Asp Ser Leu Ala Leu Ala
                         115                   120                   125
     Arg Pro Lys Ser Ser Asp Val Tyr Val Ser Tyr Asp Tyr Gly Lys Ser
                         130                   135                   140
     Phe Lys Lys Ile Ser Asp Lys Leu Asn Phe Gly Leu Gly Asn Arg Ser
                 145                   150                   155                   160
     Glu Ala Val Ile Ala Gln Phe Tyr His Ser Pro Ala Asp Asn Lys Arg
                         165                   170                   175
     Tyr Ile Phe Ala Asp Ala Tyr Ala Gln Tyr Leu Trp Ile Thr Phe Asp
                         180                   185                   190
     Phe Cys Asn Thr Leu Gln Gly Phe Ser Ile Pro Phe Arg Ala Ala Asp
                         195                   200                   205
     Leu Leu Leu His Ser Lys Ala Ser Asn Leu Leu Leu Gly Phe Asp Arg
                 210                   215                   220
     Ser His Pro Asn Lys Gln Leu Trp Lys Ser Asp Asp Phe Gly Gln Thr
          225                   230                   235                   240
     Trp Ile Met Ile Gln Glu His Val Lys Ser Phe Ser Trp Gly Ile Asp
```

42

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                     245                   250                   255
      Pro Tyr Asp Lys Pro Asn Thr Ile Tyr Ile Glu Arg His Glu Pro Ser
                 260                   265                   270
      Gly Tyr Ser Thr Val Phe Arg Ser Thr Asp Phe Phe Gln Ser Arg Glu
                 275                   280                   285
      Asn Gln Glu Val Ile Leu Glu Glu Val Arg Asp Phe Gln Leu Arg Asp
             290                   295                   300
      Lys Tyr Met Phe Ala Thr Lys Val Val His Leu Leu Gly Ser Glu Gln
      305                   310                   315                   320
      Gln Ser Ser Val Gln Leu Trp Val Ser Phe Gly Arg Lys Pro Met Arg
                     325                   330                   335
      Ala Ala Gln Phe Val Thr Arg His Pro Ile Asn Glu Tyr Tyr Ile Ala
                 340                   345                   350
      Asp Ala Ser Glu Asp Gln Val Phe Val Cys Val Ser His Ser Asn Asn
             355                   360                   365
      Arg Thr Asn Leu Tyr Ile Ser Glu Ala Glu Gly Leu Lys Phe Ser Leu
             370                   375                   380
      Ser Leu Glu Asn Val Leu Tyr Tyr Ser Pro Gly Gly Ala Gly Ser Asp
      385                   390                   395                   400
      Thr Leu Val Arg Tyr Phe Ala Asn Glu Pro Phe Ala Asp Phe His Arg
                     405                   410                   415
      Val Glu Gly Leu Gln Gly Val Tyr Ile Ala Thr Leu Ile Asn Gly Ser
                 420                   425                   430
      Met Asn Glu Glu Asn Met Arg Ser Val Ile Thr Phe Asp Lys Gly Gly
                 435                   440                   445
      Thr Trp Glu Phe Leu Gln Ala Pro Ala Phe Thr Gly Tyr Gly Glu Lys
             450                   455                   460
      Ile Asn Cys Glu Leu Ser Gln Gly Cys Ser Leu His Leu Ala Gln Arg
```

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          465                    470                    475                    480
          Leu Ser Gln Leu Leu Asn Leu Gln Leu Arg Arg Met Pro Ile Leu Ser
                              485                    490                    495
          Lys Glu Ser Ala Pro Gly Leu Ile Ile Ala Thr Gly Ser Val Gly Lys
                         500                    505                    510
          Asn Leu Ala Ser Lys Thr Asn Val Tyr Ile Ser Ser Ser Ala Gly Ala
                    515                    520                    525
          Arg Trp Arg Glu Ala Leu Pro Gly Pro His Tyr Tyr Thr Trp Gly Asp
               530                    535                    540
          His Gly Gly Ile Ile Thr Ala Ile Ala Gln Gly Met Glu Thr Asn Glu
          545                    550                    555                    560
          Leu Lys Tyr Ser Thr Asn Glu Gly Glu Thr Trp Lys Thr Phe Ile Phe
                              565                    570                    575
          Ser Glu Lys Pro Val Phe Val Tyr Gly Leu Leu Thr Glu Pro Gly Glu
                         580                    585                    590
          Lys Ser Thr Val Phe Thr Ile Phe Gly Ser Asn Lys Glu Asn Val His
                    595                    600                    605
          Ser Trp Leu Ile Leu Gln Val Asn Ala Thr Asp Ala Leu Gly Val Pro
               610                    615                    620
          Cys Thr Glu Asn Asp Tyr Lys Leu Trp Ser Pro Ser Asp Glu Arg Gly
          625                    630                    635                    640
          Asn Glu Cys Leu Leu Gly His Lys Thr Val Phe Lys Arg Arg Thr Pro
                              645                    650                    655
          His Ala Thr Cys Phe Asn Gly Glu Asp Phe Asp Arg Pro Val Val Val
                         660                    665                    670
          Ser Asn Cys Ser Cys Thr Arg Glu Asp Tyr Glu Cys Asp Phe Gly Phe
                    675                    680                    685
          Lys Met Ser Glu Asp Leu Ser Leu Glu Val Cys Val Pro Asp Pro Glu
```

44

```
              690              695              700
     Phe Ser Gly Lys Ser Tyr Ser Pro Pro Val Pro Cys Pro Val Gly Ser
     705              710              715              720
     Thr Tyr Arg Arg Thr Arg Gly Tyr Arg Lys Ile Ser Gly Asp Thr Cys
                      725              730              735
     Ser Gly Gly Asp Val Glu Ala Arg Leu Glu Gly Glu Leu Val Pro Cys
                      740              745              750
     Pro Leu Ala Glu Glu Asn Glu Phe Ile Leu Tyr Ala Val Arg Lys Ser
                      755              760              765
     Ile Tyr Arg Tyr Asp Leu Ala Ser Gly Ala Thr Glu Gln Leu Pro Leu
                      770              775              780
     Thr Gly Leu Arg Ala Ala Val Ala Leu Asp Phe Asp Tyr Glu His Asn
     785              790              795              800
     Cys Leu Tyr Trp Ser Asp Leu Ala Leu Asp Val Ile Gln Arg Leu Cys
                      805              810              815
     Leu Asn Gly Ser Thr Gly Gln Glu Val Ile Ile Asn Ser Gly Leu Glu
                      820              825              830
     Thr Val Glu Ala Leu Ala Phe Glu Pro Leu Ser Gln Leu Leu Tyr Trp
                      835              840              845
     Val Asp Ala Gly Phe Lys Lys Ile Glu Val Ala Asn Pro Asp Gly Asp
     850              855              860
     Phe Arg Leu Thr Ile Val Asn Ser Ser Val Leu Asp Arg Pro Arg Ala
     865              870              875              880
     Leu Val Leu Val Pro Gln Glu Gly Val Met Phe Trp Thr Asp Trp Gly
                      885              890              895
     Asp Leu Lys Pro Gly Ile Tyr Arg Ser Asn Met Asp Gly Ser Ala Ala
                      900              905              910
     Tyr His Leu Val Ser Glu Asp Val Lys Trp Pro Asn Gly Ile Ser Val
```

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              915                   920                   925
    Asp Asp Gln Trp Ile Tyr Trp Thr Asp Ala Tyr Leu Glu Cys Ile Glu
              930                   935                   940
    Arg Ile Thr Phe Ser Gly Gln Gln Arg Ser Val Ile Leu Asp Asn Leu
    945                   950                   955                   960
    Pro His Pro Tyr Ala Ile Ala Val Phe Lys Asn Glu Ile Tyr Trp Asp
                        965                   970                   975
    Asp Trp Ser Gln Leu Ser Ile Phe Arg Ala Ser Lys Tyr Ser Gly Ser
                        980                   985                   990
    Gln Met Glu Ile Leu Ala Asn Gln Leu Thr Gly Leu Met Asp Met Lys
                        995                  1000                  1005
    Ile Phe Tyr Lys Gly Lys Asn Thr Gly Ser Asn Ala Cys Val Pro Arg
              1010                  1015                  1020
    Pro Cys Ser Leu Leu Cys Leu Pro Lys Ala Asn Asn Ser Arg Ser Cys
    1025                  1030                  1035                  1040
    Arg Cys Pro Glu Asp Val Ser Ser Ser Val Leu Pro Ser Gly Asp Leu
                        1045                  1050                  1055
    Met Cys Asp Cys Pro Gln Gly Tyr Gln Leu Lys Asn Asn Thr Cys Val
                        1060                  1065                  1070
    Lys Glu Glu Asn Thr Cys Leu Arg Asn Gln Tyr Arg Cys Ser Asn Gly
              1075                  1080                  1085
    Asn Cys Ile Asn Ser Ile Trp Trp Cys Asp Phe Asp Asn Asp Cys Gly
              1090                  1095                  1100
    Asp Met Ser Asp Glu Arg Asn Cys Pro Thr Thr Ile Cys Asp Leu Asp
    1105                  1110                  1115                  1120
    Thr Gln Phe Arg Cys Gln Glu Ser Gly Thr Cys Ile Pro Leu Ser Tyr
                        1125                  1130                  1135
    Lys Cys Asp Leu Glu Asp Asp Cys Gly Asp Asn Ser Asp Glu Ser His
```

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                1140              1145              1150
Cys Glu Met His Gln Cys Arg Ser Asp Glu Tyr Asn Cys Ser Ser Gly
                1155              1160              1165
Met Cys Ile Arg Ser Ser Trp Val Cys Asp Gly Asp Asn Asp Cys Arg
                1170              1175              1180
Asp Trp Ser Asp Glu Ala Asn Cys Thr Ala Ile Tyr His Thr Cys Glu
1185              1190              1195              1200
Ala Ser Asn Phe Gln Cys Arg Asn Gly His Cys Ile Pro Gln Arg Trp
                1205              1210              1215
Ala Cys Asp Gly Asp Thr Asp Cys Gln Asp Gly Ser Asp Glu Asp Pro
                1220              1225              1230
Val Asn Cys Glu Lys Lys Cys Asn Gly Phe Arg Cys Pro Asn Gly Thr
                1235              1240              1245
Cys Ile Pro Ser Ser Lys His Cys Asp Gly Leu Arg Asp Cys Ser Asp
                1250              1255              1260
Gly Ser Asp Glu Gln His Cys Glu Pro Leu Cys Thr His Phe Met Asp
1265              1270              1275              1280
Phe Val Cys Lys Asn Arg Gln Gln Cys Leu Phe His Ser Met Val Cys
                1285              1290              1295
Asp Gly Ile Ile Gln Cys Arg Asp Gly Ser Asp Glu Asp Ala Ala Phe
                1300              1305              1310
Ala Gly Cys Ser Gln Asp Pro Glu Phe His Lys Val Cys Asp Glu Phe
                1315              1320              1325
Gly Phe Gln Cys Gln Asn Gly Val Cys Ile Ser Leu Ile Trp Lys Cys
                1330              1335              1340
Asp Gly Met Asp Asp Cys Gly Asp Tyr Ser Asp Glu Ala Asn Cys Glu
1345              1350              1355              1360
Asn Pro Thr Glu Ala Pro Asn Cys Ser Arg Tyr Phe Gln Phe Arg Cys
```

1365 1370 1375
Glu Asn Gly His Cys Ile Pro Asn Arg Trp Lys Cys Asp Arg Glu Asn

1380 1385 1390
Asp Cys Gly Asp Trp Ser Asp Glu Lys Asp Cys Gly Asp Ser His Ile

1395 1400 1405
Leu Pro Phe Ser Thr Pro Gly Pro Ser Thr Cys Leu Pro Asn Tyr Tyr

1410 1415 1420
Arg Cys Ser Ser Gly Thr Cys Val Met Asp Thr Trp Val Cys Asp Gly

1425 1430 1435 1440
Tyr Arg Asp Cys Ala Asp Gly Ser Asp Glu Glu Ala Cys Pro Leu Leu

1445 1450 1455
Ala Asn Val Thr Ala Ala Ser Thr Pro Thr Gln Leu Gly Arg Cys Asp

1460 1465 1470
Arg Phe Glu Phe Glu Cys His Gln Pro Lys Thr Cys Ile Pro Asn Trp

1475 1480 1485
Lys Arg Cys Asp Gly His Gln Asp Cys Gln Asp Gly Arg Asp Glu Ala

1490 1495 1500
Asn Cys Pro Thr His Ser Thr Leu Thr Cys Met Ser Arg Glu Phe Gln

1505 1510 1515 1520
Cys Glu Asp Gly Glu Ala Cys Ile Val Leu Ser Glu Arg Cys Asp Gly

1525 1530 1535
Phe Leu Asp Cys Ser Asp Glu Ser Asp Glu Lys Ala Cys Ser Asp Glu

1540 1545 1550
Leu Thr Val Tyr Lys Val Gln Asn Leu Gln Trp Thr Ala Asp Phe Ser

1555 1560 1565
Gly Asp Val Thr Leu Thr Trp Met Arg Pro Lys Lys Met Pro Ser Ala

1570 1575 1580
Ser Cys Val Tyr Asn Val Tyr Tyr Arg Val Val Gly Glu Ser Ile Trp

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        1585              1590              1595              1600
        Lys Thr Leu Glu Thr His Ser Asn Lys Thr Asn Thr Val Leu Lys Val
                          1605              1610              1615
        Leu Lys Pro Asp Thr Thr Tyr Gln Val Lys Val Gln Val Gln Cys Leu
                          1620              1625              1630
        Ser Lys Ala His Asn Thr Asn Asp Phe Val Thr Leu Arg Thr Pro Glu
                    1635              1640              1645
        Gly Leu Pro Asp Ala Pro Arg Asn Leu Gln Leu Ser Leu Pro Arg Glu
                    1650              1655              1660
        Ala Glu Gly Val Ile Val Gly His Trp Ala Pro Pro Ile His Thr His
        1665              1670              1675              1680
        Gly Leu Ile Arg Glu Tyr Ile Val Glu Tyr Ser Arg Ser Gly Ser Lys
                          1685              1690              1695
        Met Trp Ala Ser Gln Arg Ala Ala Ser Asn Phe Thr Glu Ile Lys Asn
                    1700              1705              1710
        Leu Leu Val Asn Thr Leu Tyr Thr Val Arg Val Ala Ala Val Thr Ser
                    1715              1720              1725
        Arg Gly Ile Gly Asn Trp Ser Asp Ser Lys Ser Ile Thr Thr Ile Lys
                    1730              1735              1740
        Gly Lys Val Ile Pro Pro Pro Asp Ile His Ile Asp Ser Tyr Gly Glu
        1745              1750              1755              1760
        Asn Tyr Leu Ser Phe Thr Leu Thr Met Glu Ser Asp Ile Lys Val Asn
                          1765              1770              1775
        Gly Tyr Val Val Asn Leu Phe Trp Ala Phe Asp Thr His Lys Gln Glu
                    1780              1785              1790
        Arg Arg Thr Leu Asn Phe Arg Gly Ser Ile Leu Ser His Lys Val Gly
                    1795              1800              1805
        Asn Leu Thr Ala His Thr Ser Tyr Glu Ile Ser Ala Trp Ala Lys Thr
```

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            1810                1815                1820
Asp Leu Gly Asp Ser Pro Leu Ala Phe Glu His Val Met Thr Arg Gly
    1825              1830                1835                1840
Val Arg Pro Pro Ala Pro Ser Leu Lys Ala Lys Ala Ile Asn Gln Thr
                    1845                1850                1855
Ala Val Glu Cys Thr Trp Thr Gly Pro Arg Asn Val Val Tyr Gly Ile
            1860                1865                1870
Phe Tyr Ala Thr Ser Phe Leu Asp Leu Tyr Arg Asn Pro Lys Ser Leu
            1875                1880                1885
Thr Thr Ser Leu His Asn Lys Thr Val Ile Val Ser Lys Asp Glu Gln
        1890                1895                1900
Tyr Leu Phe Leu Val Arg Val Val Val Pro Tyr Gln Gly Pro Ser Ser
    1905                1910                1915                1920
Asp Tyr Val Val Val Lys Met Ile Pro Asp Ser Arg Leu Pro Pro Arg
                1925                1930                1935
His Leu His Val Val His Thr Gly Lys Thr Ser Val Val Ile Lys Trp
            1940                1945                1950
Glu Ser Pro Tyr Asp Ser Pro Asp Gln Asp Leu Leu Tyr Ala Ile Ala
            1955                1960                1965
Val Lys Asp Leu Ile Arg Lys Thr Asp Arg Ser Tyr Lys Val Lys Ser
        1970                1975                1980
Arg Asn Ser Thr Val Glu Tyr Thr Leu Asn Lys Leu Glu Pro Gly Gly
    1985                1990                1995                2000
Lys Tyr His Ile Ile Val Gln Leu Gly Asn Met Ser Lys Asp Ser Ser
                2005                2010                2015
Ile Lys Ile Thr Thr Val Ser Leu Ser Ala Pro Asp Ala Leu Lys Ile
                2020                2025                2030
Ile Thr Glu Asn Asp His Val Leu Leu Phe Trp Lys Ser Leu Ala Leu
```

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                2035                    2040                    2045
        Lys Glu Lys His Phe Asn Glu Ser Arg Gly Tyr Glu Ile His Met Phe
            2050                    2055                    2060
        Asp Ser Ala Met Asn Ile Thr Ala Tyr Leu Gly Asn Thr Thr Asp Asn
        2065                    2070                    2075                    2080
        Phe Phe Lys Ile Ser Asn Leu Lys Met Gly His Asn Tyr Thr Phe Thr
                        2085                    2090                    2095
        Val Gln Ala Arg Cys Leu Phe Gly Asn Gln Ile Cys Gly Glu Pro Ala
                    2100                    2105                    2110
        Ile Leu Leu Tyr Asp Glu Leu Gly Ser Gly Ala Asp Ala Ser Ala Thr
                    2115                    2120                    2125
        Gln Ala Ala Arg Ser Thr Asp Val Ala Ala Val Val Val Pro Ile Leu
                2130                    2135                    2140
        Phe Leu Ile Leu Leu Ser Leu Gly Val Gly Phe Ala Ile Leu Tyr Thr
        2145                    2150                    2155                    2160
        Lys His Arg Arg Leu Gln Ser Ser Phe Thr Ala Phe Ala Asn Ser His
                        2165                    2170                    2175
        Tyr Ser Ser Arg Leu Gly Ser Ala Ile Phe Ser Ser Gly Asp Asp Leu
                    2180                    2185                    2190
        Gly Glu Asp Asp Glu Asp Ala Pro Met Ile Thr Gly Phe Ser Asp Asp
                2195                    2200                    2205
        Val Pro Met Val Ile Ala
            2210
```

Sequence ID No. 7

Length of the Sequence: 6843

Type: nucleic acid

Strandedness: double

Topology: linear

Molecular type: cDNA to mRNA

Feature:

Name/Key: sig peptide

Location: 81..164

Identification method: S

Name/Key: mat peptide

Location: 165..6722

Identification method: S

Sequence:

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                                  CCG GCCCAGCGGC TCTCCTGGCC    23
TCGCGCTGCA CATTCTCTCC TGGCGGCGGC GCCACCTGCA GTAGCGTTCG CCCGAACATG    83
                                                             Met
                                                              1
GCG ACA CGG AGC AGC AGG AGG GAG TCG CGA CTC CCG TTC CTA TTC ACC    131
Ala Thr Arg Ser Ser Arg Arg Glu Ser Arg Leu Pro Phe Leu Phe Thr
             5                  10                  15
CTG GTC GCA CTG CTG CCG CCC GGA GCT CTC TGC GAA GTC TGG ACG CAG    179
Leu Val Ala Leu Leu Pro Pro Gly Ala Leu Cys Glu Val Trp Thr Gln
             20                 25                  30
AGG CTG CAC GGC GGC AGC GCG CCC TTG CCC CAG GAC CGG GGC TTC CTC    227
Arg Leu His Gly Gly Ser Ala Pro Leu Pro Gln Asp Arg Gly Phe Leu
             35                 40                  45
GTG GTG CAG GGC GAC CCG CGC GAG CTG CGG CTG TGG GCG CGC GGG GAT    275
Val Val Gln Gly Asp Pro Arg Glu Leu Arg Leu Trp Ala Arg Gly Asp
    50                  55                  60                  65
GCC AGG GGG GCG AGC CGC GCG GAC GAG AAG CCG CTC CGG AGG AAA CGG    323
Ala Arg Gly Ala Ser Arg Ala Asp Glu Lys Pro Leu Arg Arg Lys Arg
                 70                  75                  80
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AGC GCT GCC CTG CAG CCC GAG CCC ATC AAG GTG TAC GGA CAG GTT AGT   371
Ser Ala Ala Leu Gln Pro Glu Pro Ile Lys Val Tyr Gly Gln Val Ser
           85   90   95

CTG AAT GAT TCC CAC AAT CAG ATG GTG GTG CAC TGG GCT GGA GAG AAA   419
Leu Asn Asp Ser His Asn Gln Met Val Val His Trp Ala Gly Glu Lys
           100   105   110

AGC AAC GTG ATC GTG GCC TTG GCC CGA GAT AGC CTG GCA TTG GCG AGG   467
Ser Asn Val Ile Val Ala Leu Ala Arg Asp Ser Leu Ala Leu Ala Arg
          115   120   125

CCC AAG AGC AGT GAT GTG TAC GTG TCT TAC GAC TAT GGA AAA TCA TTC   515
Pro Lys Ser Ser Asp Val Tyr Val Ser Tyr Asp Tyr Gly Lys Ser Phe
130   135   140   145

AAG AAA ATT TCA GAC AAG TTA AAC TTT GGC TTG GGA AAT AGG AGT GAA   563
Lys Lys Ile Ser Asp Lys Leu Asn Phe Gly Leu Gly Asn Arg Ser Glu
           150   155   160

GCT GTT ATC GCC CAG TTC TAC CAC AGC CCT GCG GAC AAC AAG CGG TAC   611
Ala Val Ile Ala Gln Phe Tyr His Ser Pro Ala Asp Asn Lys Arg Tyr
          165   170   175

ATC TTT GCA GAC GCT TAT GCC CAG TAC CTC TGG ATC ACG TTT GAC TTC   659
Ile Phe Ala Asp Ala Tyr Ala Gln Tyr Leu Trp Ile Thr Phe Asp Phe
           180   185   190

TGC AAC ACT CTT CAA GGC TTT TCC ATC CCA TTT CGG GCA GCT GAT CTC   707
Cys Asn Thr Leu Gln Gly Phe Ser Ile Pro Phe Arg Ala Ala Asp Leu
          195   200   205

CTC CTA CAC AGT AAG GCC TCC AAC CTT CTC TTG GGC TTT GAC AGG TCC   755
Leu Leu His Ser Lys Ala Ser Asn Leu Leu Leu Gly Phe Asp Arg Ser
210   215   220   225

CAC CCC AAC AAG CAG CTG TGG AAG TCA GAT GAC TTT GGC CAG ACC TGG   803

His Pro Asn Lys Gln Leu Trp Lys Ser Asp Asp Phe Gly Gln Thr Trp
                  230   235   240

ATC ATG ATT CAG GAA CAT GTC AAG TCC TTT TCT TGG GGA ATT GAT CCC   851
Ile Met Ile Gln Glu His Val Lys Ser Phe Ser Trp Gly Ile Asp Pro
                  245   250   255

TAT GAC AAA CCA AAT ACC ATC TAC ATT GAA CGA CAC GAA CCC TCT GGC   899
Tyr Asp Lys Pro Asn Thr Ile Tyr Ile Glu Arg His Glu Pro Ser Gly
              260   265   270

TAC TCC ACT GTC TTC CGA AGT ACA GAT TTC TTC CAG TCC CGG GAA AAC   947
Tyr Ser Thr Val Phe Arg Ser Thr Asp Phe Phe Gln Ser Arg Glu Asn
        275   280   285

CAG GAA GTG ATC CTT GAG GAA GTG AGA GAT TTT CAG CTT CGG GAC AAG   995
Gln Glu Val Ile Leu Glu Glu Val Arg Asp Phe Gln Leu Arg Asp Lys
290   295   300   305

TAC ATG TTT GCT ACA AAG GTG GTG CAT CTC TTG GGC AGT GAA CAG CAG   1043
Tyr Met Phe Ala Thr Lys Val Val His Leu Leu Gly Ser Glu Gln Gln
              310   315   320

TCT TCT GTC CAG CTC TGG GTC TCC TTT GGC CGG AAG CCC ATG AGA GCA   1091
Ser Ser Val Gln Leu Trp Val Ser Phe Gly Arg Lys Pro Met Arg Ala
         325   330   335

GCC CAG TTT GTC ACA AGA CAT CCT ATT AAT GAA TAT TAC ATC GCA GAT   1139
Ala Gln Phe Val Thr Arg His Pro Ile Asn Glu Tyr Tyr Ile Ala Asp
        340   345   350

GCC TCC GAG GAC CAG GTG TTT GTG TGT GTC AGC CAC AGT AAC AAC CGC   1187
Ala Ser Glu Asp Gln Val Phe Val Cys Val Ser His Ser Asn Asn Arg
        355   360   365

ACC AAT TTA TAC ATC TCA GAG GCA GAG GGG CTG AAG TTC TCC CTG TCC   1235
Thr Asn Leu Tyr Ile Ser Glu Ala Glu Gly Leu Lys Phe Ser Leu Ser

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         370                   375                   380                   385
       TTG GAG AAC GTG CTC TAT TAC AGC CCA GGA GGG GCC GGC AGT GAC ACC      1283
       Leu Glu Asn Val Leu Tyr Tyr Ser Pro Gly Gly Ala Gly Ser Asp Thr
                        390                   395                   400
       TTG GTG AGG TAT TTT GCA AAT GAA CCA TTT GCT GAC TTC CAC CGA GTG      1331
       Leu Val Arg Tyr Phe Ala Asn Glu Pro Phe Ala Asp Phe His Arg Val
                   405                   410                   415
       GAA GGA TTG CAA GGA GTC TAC ATT GCT ACT CTG ATT AAT GGT TCT ATG      1379
       Glu Gly Leu Gln Gly Val Tyr Ile Ala Thr Leu Ile Asn Gly Ser Met
                   420                   425                   430
       AAT GAG GAG AAC ATG AGA TCG GTC ATC ACC TTT GAC AAA GGG GGA ACC      1427
       Asn Glu Glu Asn Met Arg Ser Val Ile Thr Phe Asp Lys Gly Gly Thr
              435                   440                   445
       TGG GAG TTT CTT CAG GCT CCA GCC TTC ACG GGA TAT GGA GAG AAA ATC      1475
       Trp Glu Phe Leu Gln Ala Pro Ala Phe Thr Gly Tyr Gly Glu Lys Ile
       450                   455                   460                   465
       AAT TGT GAG CTT TCC CAG GGC TGT TCC CTT CAT CTG GCT CAG CGC CTC      1523
       Asn Cys Glu Leu Ser Gln Gly Cys Ser Leu His Leu Ala Gln Arg Leu
                        470                   475                   480
       AGT CAG CTC CTC AAC CTC CAG CTC CGG AGA ATG CCC ATC CTG TCC AAG      1571
       Ser Gln Leu Leu Asn Leu Gln Leu Arg Arg Met Pro Ile Leu Ser Lys
                   485                   490                   495
       GAG TCG GCT CCA GGC CTC ATC ATC GCC ACT GGC TCA GTG GGA AAG AAC      1619
       Glu Ser Ala Pro Gly Leu Ile Ile Ala Thr Gly Ser Val Gly Lys Asn
                   500                   505                   510
       TTG GCT AGC AAG ACA AAC GTG TAC ATC TCT AGC AGT GCT GGA GCC AGG      1667
       Leu Ala Ser Lys Thr Asn Val Tyr Ile Ser Ser Ser Ala Gly Ala Arg
              515                   520                   525
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TGG CGA GAG GCA CTT CCT GGA CCT CAC TAC TAC ACA TGG GGA GAC CAC   1715
Trp Arg Glu Ala Leu Pro Gly Pro His Tyr Tyr Thr Trp Gly Asp His
530   535   540   545

GGC GGA ATC ATC ACG GCC ATT GCC CAG GGC ATG GAA ACC AAC GAG CTA   1763
Gly Gly Ile Ile Thr Ala Ile Ala Gln Gly Met Glu Thr Asn Glu Leu
          550   555   560

AAA TAC AGT ACC AAT GAA GGG GAG ACC TGG AAA ACA TTC ATC TTC TCT   1811
Lys Tyr Ser Thr Asn Glu Gly Glu Thr Trp Lys Thr Phe Ile Phe Ser
          565   570   575

GAG AAG CCA GTG TTT GTG TAT GGC CTC CTC ACA GAA CCT GGG GAG AAG   1859
Glu Lys Pro Val Phe Val Tyr Gly Leu Leu Thr Glu Pro Gly Glu Lys
          580   585   590

AGC ACT GTC TTC ACC ATC TTT GGC TCG AAC AAA GAG AAT GTC CAC AGC   1907
Ser Thr Val Phe Thr Ile Phe Gly Ser Asn Lys Glu Asn Val His Ser
       595   600   605

TGG CTG ATC CTC CAG GTC AAT GCC ACG GAT GCC TTG GGA GTT CCC TGC   1955
Trp Leu Ile Leu Gln Val Asn Ala Thr Asp Ala Leu Gly Val Pro Cys
610   615   620   625

ACA GAG AAT GAC TAC AAG CTG TGG TCA CCA TCT GAT GAG CGG GGG AAT   2003
Thr Glu Asn Asp Tyr Lys Leu Trp Ser Pro Ser Asp Glu Arg Gly Asn
          630   635   640

GAG TGT TTG CTG GGA CAC AAG ACT GTT TTC AAA CGG CGG ACC CCC CAT   2051
Glu Cys Leu Leu Gly His Lys Thr Val Phe Lys Arg Arg Thr Pro His
          645   650   655

GCC ACA TGC TTC AAT GGA GAG GAC TTT GAC AGG CCG GTG GTC GTG TCC   2099
Ala Thr Cys Phe Asn Gly Glu Asp Phe Asp Arg Pro Val Val Val Ser
          660   665   670

AAC TGC TCC TGC ACC CGG GAG GAC TAT GAG TGT GAC TTC GGT TTC AAG   2147

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          Asn Cys Ser Cys Thr Arg Glu Asp Tyr Glu Cys Asp Phe Gly Phe Lys
             675             680             685

ATG AGT GAA GAT TTG TCA TTA GAG GTT TGT GTT CCA GAT CCG GAA TTT    2195
Met Ser Glu Asp Leu Ser Leu Glu Val Cys Val Pro Asp Pro Glu Phe
690           695             700             705

TCT GGA AAG TCA TAC TCC CCT CCT GTG CCT TGC CCT GTG GGT TCT ACT    2243
Ser Gly Lys Ser Tyr Ser Pro Pro Val Pro Cys Pro Val Gly Ser Thr
             710             715             720

TAC AGG AGA ACG AGA GGC TAC CGG AAG ATT TCT GGG GAC ACT TGT AGC    2291
Tyr Arg Arg Thr Arg Gly Tyr Arg Lys Ile Ser Gly Asp Thr Cys Ser
                 725             730             735

GGA GGA GAT GTT GAA GCG CGA CTG GAA GGA GAG CTG GTC CCC TGT CCC    2339
Gly Gly Asp Val Glu Ala Arg Leu Glu Gly Glu Leu Val Pro Cys Pro
             740             745             750

CTG GCA GAA GAG AAC GAG TTC ATT CTG TAT GCT GTG AGG AAA TCC ATC    2387
Leu Ala Glu Glu Asn Glu Phe Ile Leu Tyr Ala Val Arg Lys Ser Ile
     755             760             765

TAC CGC TAT GAC CTG GCC TCG GGA GCC ACC GAG CAG TTG CCT CTC ACC    2435
Tyr Arg Tyr Asp Leu Ala Ser Gly Ala Thr Glu Gln Leu Pro Leu Thr
770             775             780             785

GGG CTA CGG GCA GCA GTG GCC CTG GAC TTT GAC TAT GAG CAC AAC TGT    2483
Gly Leu Arg Ala Ala Val Ala Leu Asp Phe Asp Tyr Glu His Asn Cys
             790             795             800

TTG TAT TGG TCC GAC CTG GCC TTG GAC GTC ATC CAG CGC CTC TGT TTG    2531
Leu Tyr Trp Ser Asp Leu Ala Leu Asp Val Ile Gln Arg Leu Cys Leu
             805             810             815

AAT GGA AGC ACA GGG CAA GAG GTG ATC ATC AAT TCT GGC CTG GAG ACA    2579
Asn Gly Ser Thr Gly Gln Glu Val Ile Ile Asn Ser Gly Leu Glu Thr
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<pre>
          820   825   830
    GTA GAA GCT TTG GCT TTT GAA CCC CTC AGC CAG CTG CTT TAC TGG GTA   2627
    Val Glu Ala Leu Ala Phe Glu Pro Leu Ser Gln Leu Leu Tyr Trp Val
          835   840   845
    GAT GCA GGC TTC AAA AAG ATT GAG GTA GCT AAT CCA GAT GGC GAC TTC   2675
    Asp Ala Gly Phe Lys Lys Ile Glu Val Ala Asn Pro Asp Gly Asp Phe
    850   855   860   865
    CGA CTC ACA ATC GTC AAT TCC TCT GTG CTT GAT CGT CCC AGG GCT CTG   2723
    Arg Leu Thr Ile Val Asn Ser Ser Val Leu Asp Arg Pro Arg Ala Leu
                      870   875   880
    GTC CTC GTG CCC CAA GAG GGG GTG ATG TTC TGG ACA GAC TGG GGA GAC   2771
    Val Leu Val Pro Gln Glu Gly Val Met Phe Trp Thr Asp Trp Gly Asp
                      885   890   895
    CTG AAG CCT GGG ATT TAT CGG AGC AAT ATG GAT GGT TCT GCT GCC TAT   2819
    Leu Lys Pro Gly Ile Tyr Arg Ser Asn Met Asp Gly Ser Ala Ala Tyr
              900   905   910
    CAC CTG GTG TCT GAG GAT GTG AAG TGG CCC AAT GGC ATC TCT GTG GAC   2867
    His Leu Val Ser Glu Asp Val Lys Trp Pro Asn Gly Ile Ser Val Asp
          915   920   925
    GAC CAG TGG ATT TAC TGG ACG GAT GCC TAC CTG GAG TGC ATA GAG CGG   2915
    Asp Gln Trp Ile Tyr Trp Thr Asp Ala Tyr Leu Glu Cys Ile Glu Arg
    930   935   940   945
    ATC ACG TTC AGT GGC CAG CAG CGC TCT GTC ATT CTG GAC AAC CTC CCG   2963
    Ile Thr Phe Ser Gly Gln Gln Arg Ser Val Ile Leu Asp Asn Leu Pro
                      950   955   960
    CAC CCC TAT GCC ATT GCT GTC TTT AAG AAT GAA ATC TAC TGG GAT GAC   3011
    His Pro Tyr Ala Ile Ala Val Phe Lys Asn Glu Ile Tyr Trp Asp Asp
                      965   970   975
</pre>

TGG TCA CAG CTC AGC ATA TTC CGA GCT TCC AAA TAC AGT GGG TCC CAG   3059
Trp Ser Gln Leu Ser Ile Phe Arg Ala Ser Lys Tyr Ser Gly Ser Gln
        980   985   990

ATG GAG ATT CTG GCA AAC CAG CTC ACG GGG CTC ATG GAC ATG AAG ATT   3107
Met Glu Ile Leu Ala Asn Gln Leu Thr Gly Leu Met Asp Met Lys Ile
        995   1000   1005

TTC TAC AAG GGG AAG AAC ACT GGA AGC AAT GCC TGT GTG CCC AGG CCA   3155
Phe Tyr Lys Gly Lys Asn Thr Gly Ser Asn Ala Cys Val Pro Arg Pro
1010   1015   1020   1025

TGC AGC CTG CTG TGC CTG CCC AAG GCC AAC AAC AGT AGA AGC TGC AGG   3203
Cys Ser Leu Leu Cys Leu Pro Lys Ala Asn Asn Ser Arg Ser Cys Arg
                1030   1035   1040

TGT CCA GAG GAT GTG TCC AGC AGT GTG CTT CCA TCA GGG GAC CTG ATG   3251
Cys Pro Glu Asp Val Ser Ser Ser Val Leu Pro Ser Gly Asp Leu Met
                1045   1050   1055

TGT GAC TGC CCT CAG GGC TAT CAG CTC AAG AAC AAT ACC TGT GTC AAA   3299
Cys Asp Cys Pro Gln Gly Tyr Gln Leu Lys Asn Asn Thr Cys Val Lys
            1060   1065   1070

GAA GAG AAC ACC TGT CTT CGC AAC CAG TAT CGC TGC AGC AAC GGG AAC   3347
Glu Glu Asn Thr Cys Leu Arg Asn Gln Tyr Arg Cys Ser Asn Gly Asn
        1075   1080   1085

TGT ATC AAC AGC ATT TGG TGG TGT GAC TTT GAC AAC GAC TGT GGA GAC   3395
Cys Ile Asn Ser Ile Trp Trp Cys Asp Phe Asp Asn Asp Cys Gly Asp
1090   1095   1100   1105

ATG AGC GAT GAG AGA AAC TGC CCT ACC ACC ATC TGT GAC CTG GAC ACC   3443
Met Ser Asp Glu Arg Asn Cys Pro Thr Thr Ile Cys Asp Leu Asp Thr
                1110   1115   1120

CAG TTT CGT TGC CAG GAG TCT GGG ACT TGT ATC CCA CTG TCC TAT AAA   3491

Gln Phe Arg Cys Gln Glu Ser Gly Thr Cys Ile Pro Leu Ser Tyr Lys
           1125   1130   1135

TGT GAC CTT GAG GAT GAC TGT GGA GAC AAC AGT GAT GAA AGT CAT TGT   3539
Cys Asp Leu Glu Asp Asp Cys Gly Asp Asn Ser Asp Glu Ser His Cys
           1140   1145   1150

GAA ATG CAC CAG TGC CGG AGT GAC GAG TAC AAC TGC AGT TCC GGC ATG   3587
Glu Met His Gln Cys Arg Ser Asp Glu Tyr Asn Cys Ser Ser Gly Met
           1155   1160   1165

TGC ATC CGC TCC TCC TGG GTA TGT GAC GGG GAC AAC GAC TGC AGG GAC   3635
Cys Ile Arg Ser Ser Trp Val Cys Asp Gly Asp Asn Asp Cys Arg Asp
1170   1175   1180   1185

TGG TCT GAT GAA GCC AAC TGT ACC GCC ATC TAT CAC ACC TGT GAG GCC   3683
Trp Ser Asp Glu Ala Asn Cys Thr Ala Ile Tyr His Thr Cys Glu Ala
           1190   1195   1200

TCC AAC TTC CAG TGC CGA AAC GGG CAC TGC ATC CCC CAG CGG TGG GCG   3731
Ser Asn Phe Gln Cys Arg Asn Gly His Cys Ile Pro Gln Arg Trp Ala
           1205   1210   1215

TGT GAC GGG GAT ACG GAC TGC CAG GAT GGT TCC GAT GAG GAT CCA GTC   3779
Cys Asp Gly Asp Thr Asp Cys Gln Asp Gly Ser Asp Glu Asp Pro Val
           1220   1225   1230

AAC TGT GAG AAG AAG TGC AAT GGA TTC CGC TGC CCA AAC GGC ACT TGC   3827
Asn Cys Glu Lys Lys Cys Asn Gly Phe Arg Cys Pro Asn Gly Thr Cys
           1235   1240   1245

ATC CCA TCC AGC AAA CAT TGT GAT GGT CTG CGT GAT TGC TCT GAT GGC   3875
Ile Pro Ser Ser Lys His Cys Asp Gly Leu Arg Asp Cys Ser Asp Gly
1250   1255   1260   1265

TCC GAT GAA CAG CAC TGC GAG CCC CTC TGT ACG CAC TTC ATG GAC TTT   3923
Ser Asp Glu Gln His Cys Glu Pro Leu Cys Thr His Phe Met Asp Phe

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              1270              1275              1280
       GTG TGT AAG AAC CGC CAG CAG TGC CTG TTC CAC TCC ATG GTC TGT GAC      3971
       Val Cys Lys Asn Arg Gln Gln Cys Leu Phe His Ser Met Val Cys Asp

                 1285              1290              1295
       GGA ATC ATC CAG TGC CGC GAC GGG TCC GAT GAG GAT GCG GCG TTT GCA      4019
       Gly Ile Ile Gln Cys Arg Asp Gly Ser Asp Glu Asp Ala Ala Phe Ala

              1300              1305              1310
       GGA TGC TCC CAA GAT CCT GAG TTC CAC AAG GTA TGT GAT GAG TTC GGT      4067
       Gly Cys Ser Gln Asp Pro Glu Phe His Lys Val Cys Asp Glu Phe Gly

           1315              1320              1325
       TTC CAG TGT CAG AAT GGA GTG TGC ATC AGT TTG ATT TGG AAG TGC GAC      4115
       Phe Gln Cys Gln Asn Gly Val Cys Ile Ser Leu Ile Trp Lys Cys Asp

        1330              1335              1340              1345
       GGG ATG GAT GAT TGC GGC GAT TAT TCT GAT GAA GCC AAC TGC GAA AAC      4163
       Gly Met Asp Asp Cys Gly Asp Tyr Ser Asp Glu Ala Asn Cys Glu Asn

                  1350              1355              1360
       CCC ACA GAA GCC CCA AAC TGC TCC CGC TAC TTC CAG TTT CGG TGT GAG      4211
       Pro Thr Glu Ala Pro Asn Cys Ser Arg Tyr Phe Gln Phe Arg Cys Glu

                1365              1370              1375
       AAT GGC CAC TGC ATC CCC AAC AGA TGG AAA TGT GAC AGG GAG AAC GAC      4259
       Asn Gly His Cys Ile Pro Asn Arg Trp Lys Cys Asp Arg Glu Asn Asp

              1380              1385              1390
       TGT GGG GAC TGG TCT GAT GAG AAG GAT TGT GGA GAT TCA CAT ATT CTT      4307
       Cys Gly Asp Trp Ser Asp Glu Lys Asp Cys Gly Asp Ser His Ile Leu

           1395              1400              1405
       CCC TTC TCG ACT CCT GGG CCC TCC ACG TGT CTG CCC AAT TAC TAC CGC      4355
       Pro Phe Ser Thr Pro Gly Pro Ser Thr Cys Leu Pro Asn Tyr Tyr Arg
        1410              1415              1420              1425
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TGC AGC AGT GGG ACC TGC GTG ATG GAC ACC TGG GTG TGC GAC GGG TAC   4403
Cys Ser Ser Gly Thr Cys Val Met Asp Thr Trp Val Cys Asp Gly Tyr
             1430   1435   1440

CGA GAT TGT GCA GAT GGC TCT GAC GAG GAA GCC TGC CCC TTG CTT GCA   4451
Arg Asp Cys Ala Asp Gly Ser Asp Glu Glu Ala Cys Pro Leu Leu Ala
             1445   1450   1455

AAC GTC ACT GCT GCC TCC ACT CCC ACC CAA CTT GGG CGA TGT GAC CGA   4499
Asn Val Thr Ala Ala Ser Thr Pro Thr Gln Leu Gly Arg Cys Asp Arg
             1460   1465   1470

TTT GAG TTC GAA TGC CAC CAA CCG AAG ACG TGT ATT CCC AAC TGG AAG   4547
Phe Glu Phe Glu Cys His Gln Pro Lys Thr Cys Ile Pro Asn Trp Lys
         1475   1480   1485

CGC TGT GAC GGC CAC CAA GAT TGC CAG GAT GGC CGG GAC GAG GCC AAT   4595
Arg Cys Asp Gly His Gln Asp Cys Gln Asp Gly Arg Asp Glu Ala Asn
1490   1495   1500   1505

TGC CCC ACA CAC AGC ACC TTG ACT TGC ATG AGC AGG GAG TTC CAG TGC   4643
Cys Pro Thr His Ser Thr Leu Thr Cys Met Ser Arg Glu Phe Gln Cys
             1510   1515   1520

GAG GAC GGG GAG GCC TGC ATT GTG CTC TCG GAG CGC TGC GAC GGC TTC   4691
Glu Asp Gly Glu Ala Cys Ile Val Leu Ser Glu Arg Cys Asp Gly Phe
             1525   1530   1535

CTG GAC TGC TCG GAC GAG AGC GAT GAA AAG GCC TGC AGT GAT GAG TTG   4739
Leu Asp Cys Ser Asp Glu Ser Asp Glu Lys Ala Cys Ser Asp Glu Leu
             1540   1545   1550

ACT GTG TAC AAA GTA CAG AAT CTT CAG TGG ACA GCT GAC TTC TCT GGG   4787
Thr Val Tyr Lys Val Gln Asn Leu Gln Trp Thr Ala Asp Phe Ser Gly
         1555   1560   1565

GAT GTG ACT TTG ACC TGG ATG AGG CCC AAA AAA ATG CCC TCT GCA TCT   4835

Asp Val Thr Leu Thr Trp Met Arg Pro Lys Lys Met Pro Ser Ala Ser
1570   1575   1580   1585

TGT GTA TAT AAT GTC TAC TAC AGG GTG GTT GGA GAG AGC ATA TGG AAG   4883
Cys Val Tyr Asn Val Tyr Tyr Arg Val Val Gly Glu Ser Ile Trp Lys
            1590   1595   1600

ACT CTG GAG ACC CAC AGC AAT AAG ACA AAC ACT GTA TTA AAA GTC TTG   4931
Thr Leu Glu Thr His Ser Asn Lys Thr Asn Thr Val Leu Lys Val Leu
            1605   1610   1615

AAA CCA GAT ACC ACG TAT CAG GTT AAA GTA CAG GTT CAG TGT CTC AGC   4979
Lys Pro Asp Thr Thr Tyr Gln Val Lys Val Gln Val Gln Cys Leu Ser
        1620   1625   1630

AAG GCA CAC AAC ACC AAT GAC TTT GTG ACC CTG AGG ACC CCA GAG GGA   5027
Lys Ala His Asn Thr Asn Asp Phe Val Thr Leu Arg Thr Pro Glu Gly
      1635   1640   1645

TTG CCA GAT GCC CCT CGA AAT CTC CAG CTG TCA CTC CCC AGG GAA GCA   5075
Leu Pro Asp Ala Pro Arg Asn Leu Gln Leu Ser Leu Pro Arg Glu Ala
1650   1655   1660   1665

GAA GGT GTG ATT GTA GGC CAC TGG GCT CCT CCC ATC CAC ACC CAT GGC   5123
Glu Gly Val Ile Val Gly His Trp Ala Pro Pro Ile His Thr His Gly
            1670   1675   1680

CTC ATC CGT GAG TAC ATT GTA GAA TAC AGC AGG AGT GGT TCC AAG ATG   5171
Leu Ile Arg Glu Tyr Ile Val Glu Tyr Ser Arg Ser Gly Ser Lys Met
        1685   1690   1695

TGG GCC TCC CAG AGG GCT GCT AGT AAC TTT ACA GAA ATC AAG AAC TTA   5219
Trp Ala Ser Gln Arg Ala Ala Ser Asn Phe Thr Glu Ile Lys Asn Leu
      1700   1705   1710

TTG GTC AAC ACT CTA TAC ACC GTC AGA GTG GCT GCG GTG ACT AGT CGT   5267
Leu Val Asn Thr Leu Tyr Thr Val Arg Val Ala Ala Val Thr Ser Arg

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              1715                    1720                    1725
     GGA ATA GGA AAC TGG AGC GAT TCT AAA TCC ATT ACC ACC ATA AAA GGA     5315
     Gly Ile Gly Asn Trp Ser Asp Ser Lys Ser Ile Thr Thr Ile Lys Gly
        1730                    1735                    1740             1745
     AAA GTG ATC CCA CCA CCA GAT ATC CAC ATT GAC AGC TAT GGT GAA AAT     5363
     Lys Val Ile Pro Pro Pro Asp Ile His Ile Asp Ser Tyr Gly Glu Asn
                      1750                    1755                    1760
     TAT CTA AGC TTC ACC CTG ACC ATG GAG AGT GAT ATC AAG GTG AAT GGC     5411
     Tyr Leu Ser Phe Thr Leu Thr Met Glu Ser Asp Ile Lys Val Asn Gly
                         1765                    1770                    1775
     TAT GTG GTG AAC CTT TTC TGG GCA TTT GAC ACC CAC AAG CAA GAG AGG     5459
     Tyr Val Val Asn Leu Phe Trp Ala Phe Asp Thr His Lys Gln Glu Arg
                      1780                    1785                    1790
     AGA ACT TTG AAC TTC CGA GGA AGC ATA TTG TCA CAC AAA GTT GGC AAT     5507
     Arg Thr Leu Asn Phe Arg Gly Ser Ile Leu Ser His Lys Val Gly Asn
                 1795                    1800                    1805
     CTG ACA GCT CAT ACA TCC TAT GAG ATT TCT GCC TGG GCC AAG ACT GAC     5555
     Leu Thr Ala His Thr Ser Tyr Glu Ile Ser Ala Trp Ala Lys Thr Asp
        1810                    1815                    1820             1825
     TTG GGG GAT AGC CCT CTG GCA TTT GAG CAT GTT ATG ACC AGA GGG GTT     5603
     Leu Gly Asp Ser Pro Leu Ala Phe Glu His Val Met Thr Arg Gly Val
                          1830                    1835                    1840
     CGC CCA CCT GCA CCT AGC CTC AAG GCC AAA GCC ATC AAC CAG ACT GCA     5651
     Arg Pro Pro Ala Pro Ser Leu Lys Ala Lys Ala Ile Asn Gln Thr Ala
                   1845                    1850                    1855
     GTG GAA TGT ACC TGG ACC GGC CCC CGG AAT GTG GTT TAT GGT ATT TTC     5699
     Val Glu Cys Thr Trp Thr Gly Pro Arg Asn Val Val Tyr Gly Ile Phe
              1860                    1865                    1870
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TAT GCC ACG TCC TTT CTT GAC CTC TAT CGC AAC CCG AAG AGC TTG ACT   5747
Tyr Ala Thr Ser Phe Leu Asp Leu Tyr Arg Asn Pro Lys Ser Leu Thr
    1875   1880   1885

ACT TCA CTC CAC AAC AAG ACG GTC ATT GTC AGT AAG GAT GAG CAG TAT   5795
Thr Ser Leu His Asn Lys Thr Val Ile Val Ser Lys Asp Glu Gln Tyr
1890   1895   1900   1905

TTG TTT CTG GTC CGT GTA GTG GTA CCC TAC CAG GGG CCA TCC TCT GAC   5843
Leu Phe Leu Val Arg Val Val Val Pro Tyr Gln Gly Pro Ser Ser Asp
         1910   1915   1920

TAC GTT GTA GTG AAG ATG ATC CCG GAC AGC AGG CTT CCA CCC CGT CAC   5891
Tyr Val Val Val Lys Met Ile Pro Asp Ser Arg Leu Pro Pro Arg His
         1925   1930   1935

CTG CAT GTG GTT CAT ACG GGC AAA ACC TCC GTG GTC ATC AAG TGG GAA   5939
Leu His Val Val His Thr Gly Lys Thr Ser Val Val Ile Lys Trp Glu
         1940   1945   1950

TCA CCG TAT GAC TCT CCT GAC CAG GAC TTG TTG TAT GCA ATT GCA GTC   5987
Ser Pro Tyr Asp Ser Pro Asp Gln Asp Leu Leu Tyr Ala Ile Ala Val
     1955   1960   1965

AAA GAT CTC ATA AGA AAG ACT GAC AGG AGC TAC AAA GTA AAA TCC CGT   6035
Lys Asp Leu Ile Arg Lys Thr Asp Arg Ser Tyr Lys Val Lys Ser Arg
1970   1975   1980   1985

AAC AGC ACT GTG GAA TAC ACC CTT AAC AAG TTG GAG CCT GGC GGG AAA   6083
Asn Ser Thr Val Glu Tyr Thr Leu Asn Lys Leu Glu Pro Gly Gly Lys
         1990   1995   2000

TAC CAC ATC ATT GTC CAA CTG GGG AAC ATG AGC AAA GAT TCC AGC ATA   6131
Tyr His Ile Ile Val Gln Leu Gly Asn Met Ser Lys Asp Ser Ser Ile
         2005   2010   2015

AAA ATT ACC ACA GTT TCA TTA TCA GCA CCT GAT GCC TTA AAA ATC ATA   6179

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       Lys Ile Thr Thr Val Ser Leu Ser Ala Pro Asp Ala Leu Lys Ile Ile
            2020              2025              2030

       ACA GAA AAT GAT CAT GTT CTT CTG TTT TGG AAA AGC CTG GCT TTA AAG    6227
       Thr Glu Asn Asp His Val Leu Leu Phe Trp Lys Ser Leu Ala Leu Lys
            2035              2040              2045

       GAA AAG CAT TTT AAT GAA AGC AGG GGC TAT GAG ATA CAC ATG TTT GAT    6275
       Glu Lys His Phe Asn Glu Ser Arg Gly Tyr Glu Ile His Met Phe Asp
       2050              2055              2060              2065

       AGT GCC ATG AAT ATC ACA GCT TAC CTT GGG AAT ACT ACT GAC AAT TTC    6323.
       Ser Ala Met Asn Ile Thr Ala Tyr Leu Gly Asn Thr Thr Asp Asn Phe
                      2070              2075              2080

       TTT AAA ATT TCC AAC CTG AAG ATG GGT CAT AAT TAC ACG TTC ACC GTC    6371
       Phe Lys Ile Ser Asn Leu Lys Met Gly His Asn Tyr Thr Phe Thr Val
                 2085              2090              2095

       CAA GCA AGA TGC CTT TTT GGC AAC CAG ATC TGT GGG GAG CCT GCC ATC    6419
       Gln Ala Arg Cys Leu Phe Gly Asn Gln Ile Cys Gly Glu Pro Ala Ile
            2100              2105              2110

       CTG CTG TAC GAT GAG CTG GGG TCT GGT GCA GAT GCA TCT GCA ACG CAG    6467
       Leu Leu Tyr Asp Glu Leu Gly Ser Gly Ala Asp Ala Ser Ala Thr Gln
            2115              2120              2125

       GCT GCC AGA TCT ACG GAT GTT GCT GCT GTG GTG GTG CCC ATC TTA TTC    6515
       Ala Ala Arg Ser Thr Asp Val Ala Ala Val Val Val Pro Ile Leu Phe
       2130              2135              2140              2145

       CTG ATA CTG CTG AGC CTG GGG GTG GGG TTT GCC ATC CTG TAC ACG AAG    6563
       Leu Ile Leu Leu Ser Leu Gly Val Gly Phe Ala Ile Leu Tyr Thr Lys
                 2150              2155              2160

       CAC CGG AGG CTG CAG AGC AGC TTC ACC GCC TTC GCC AAC AGC CAC TAC    6611
       His Arg Arg Leu Gln Ser Ser Phe Thr Ala Phe Ala Asn Ser His Tyr
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          2165                2170                2175
AGC TCC AGG CTG GGG TCC GCA ATC TTC TCC TCT GGG GAT GAC CTG GGG    6659
Ser Ser Arg Leu Gly Ser Ala Ile Phe Ser Ser Gly Asp Asp Leu Gly

          2180                2185                2190
GAA GAT GAT GAA GAT GCC CCT ATG ATA ACT GGA TTT TCA GAT GAC GTC    6707
Glu Asp Asp Glu Asp Ala Pro Met Ile Thr Gly Phe Ser Asp Asp Val

          2195                2200                2205
CCC ATG GTG ATA GCC TGAAAGAGCT TTCCTCACTA GAAACCAAAT GGTGTAAATA    6762
Pro Met Val Ile Ala

2210
TTTTATTTGA TAAAGATAGT TGATGGTTTA TTTTAAAAGA TGCACTTTGA GTTGCAATAT    6822

GTTATTTTTA TATGGGCCAA A    6843
```

SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:
        (A) NAME: KOWA CO., LTD.
        (B) STREET: 6-29, Nishiki 3-chome, Naka-ku, Nagoya-shi,
        (C) CITY: Aichi
        (E) COUNTRY: Japan
        (F) POSTAL CODE (ZIP): none

    (ii) TITLE OF INVENTION: NOVEL LDL RECEPTOR ANALOG PROTEIN AND THE
        GENE CODING THEREFOR

    (iii) NUMBER OF SEQUENCES: 7

    (iv) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6639 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA to mRNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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ATGGCGACAC GGAGCAGCAG GAGGGAGTCG CGACTCCCCT TCCTATTCAC CCTGGTCGCG      60

CTGCTGCCGC CCGGGGCTCT CTGCGAGGTG TGGACGCGGA CACTGCACGG CGGCCGCGCG     120

CCCTTACCCC AGGAGCGGGG CTTCCGCGTG GTGCAGGGCG ACCCGCGCGA GCTGCGGCTG     180

TGGGAGCGCG GGGATGCCAG GGGGGGCGAGC CGGGCGGACG AGAAGCCGCT CCGGAGGAGA    240

CGGAGCGCTG CCCTGCAGCC CGAGCCCATC AAGGTGTACG GACAGGTCAG CCTCAATGAT     300

TCCCACAATC AGATGGTGGT GCACTGGGCC GGAGAGAAAA GCAACGTGAT CGTGGCCTTG     360

GCCCGGGACA GCCTGGCGTT GGCCAGGCCC AGGAGCAGTG ATGTGTACGT GTCTTATGAC     420

TATGGAAAAT CATTCAATAA GATTTCAGAG AAAATTGAACT TCGGCGCGGG AAATAACACA    480

GAGGCTGTGG TGGCCCAGTT CTACCACAGC CCTGCGGACA ACAAACGGTA CATCTTCGCA     540

GATGCCTACG CCCAGTATCT CTGGATCACG TTTGACTTCT GCAACACCAT CCATGGCTTT     600

TCCATCCCGT TCCGGGCAGC TGATCTCCTA CTCCACAGTA AGGCCTCCAA CCTTCTCCTG     660

GGCTTCGACA GGTCTCACCC CAACAAGCAG CTGTGGAAGT CGGATGATTT TGGCCAGACC     720

TGGATCATGA TTCAAGAACA CGTGAAGTCC TTTTCTTGGG GAATTGATCC CTATGACAAA     780
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CCAAACACCA TCTACATCGA ACGGCACGAA CCTTCTGGCT ACTCCACGGT TTTCCGAAGT      840
ACAGACTTCT TCCAGTCCCG GGAAAACCAG GAAGTGATCT TGGAGGAAGT GAGAGACTTT      900
CAGCTTCGGG ACAAGTACAT GTTTGCTACA AAGGTGGTGC ATCTCTTGGG CAGTCCACTG      960
CAGTCTTCTG TCCAGCTCTG GGTCTCCTTT GGCCGGAAGC CCATGCGGGC CGCCCAGTTT     1020
GTTACAAGAC ATCCTATCAA CGAATATTAC ATCGCGGATG CCTCGGAGGA CCAGGTGTTT     1080
GTGTGTGTCA GTCACAGCAA CAACCGCACC AACCTCTACA TCTCGGAGGC AGAGGGCTTG     1140
AAGTTCTCTC TGTCCCTGGA GAACGTGCTC TACTACACCC CGGGAGGGGC CGGCAGTGAC     1200
ACCTTGGTGA GGTACTTTGC AAATGAACCG TTTGCTGACT CCATCGTGT GGAAGGGTTG      1260
CAGGGAGTCT ACATTGCTAC TCTGATTAAT GGTTCTATGA ATGAGGAGAA CATGAGATCT     1320
GTCATCACCT TTGACAAAGG GGGCACCTGG GAATTTCTGC AGGCTCCAGC CTTCACGGGG     1380
TATGGAGAGA AAATCAACTG TGAGCTGTCC GAGGGCTGTT CCCTCCACCT GGCCCAGCGC     1440
CTCAGCCAGC TGCTCAACCT CCAGCTCCGG AGGATGCCCA TCCTGTCCAA GGAGTCGGCG     1500
CCTGGCCTCA TCATTGCCAC GGGCTCAGTG GGAAAGAACT TGGCTAGCAA GACAAACGTG     1560
TACATCTCTA GCAGTGCTGG AGCCAGGTGG CGAGAGGCAC TTCCTGGACC TCACTACTAT     1620
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CTGAAGTACA GTACCAACGA AGGGGAGACC TGGAAAGCCT TCACCTTCTC TGAGAAGCCC     1740
GTGTTTGTGT ATGGGCTCCT CACGGAACCC GGCGAGAAGA GCACGGTCTT CACCATCTTT     1800
GGCTCCAACA AGGAGAACGT GCACAGCTGG CTCATCCTCC AGGTCAATGC CACAGACGCC     1860
CTGGGGGTTC CTTGCACAGA GAACGACTAC AAGCTCTGGT CACCATCTGA TGAGCGGGGG     1920
AATGAGTGTT TGCTTGGACA CAAGACTGTT TTCAAACGGA GGACCCCGCA CGCCACATGC     1980
TTTAACGGAG AAGACTTTGA CAGGCCGGTG GTTGTGTCCA ACTGCTCCTG CACCCGGGAG     2040
GACTATGAGT GTGACTTTGG CTTCCGGATG AGTGAAGACT TGGCATTAGA GGTGTGTGTT     2100
CCAGATCCAG GATTTTCTGG AAAGTCCTCC CCTCCAGTGC CTTGTCCCGT GGGCTCTACG     2160
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GAGGCACGGC TAGAAGGAGA GCTGGTCCCC TGTCCCCTGG CAGAAGAGAA CGAGTTCATC     2280
CTGTACGCCA CGCGCAAGTC CATCCACCGC TATGACCTGG CTTCCGGAAC CACGGAGCAG     2340
TTGCCCCTCA CTGGGTTGCG GGCAGCAGTG GCCCTGGACT TTGACTATGA GCACAACTGC     2400
CTGTATTGGT CTGACCTGGC CTTGGACGTC ATCCAGCGCC TCTGTTTGAA CGGGAGTACA     2460
GGACAAGAGG TGATCATCAA CTCTGACCTG GAGACGGTAG AAGCTTTGGC TTTTGAACCC     2520
CTCAGCCAAT TACTTTACTG GGTGGACGCA GGCTTTAAAA AGATCGAGGT AGCCAATCCA     2580
GATGGTGACT TCCGACTCAC CGTCGTCAAT TCCTCGGTGC TGGATCGGCC CCGGGCCCTG     2640
GTCCTTGTGC CCCAAGAAGG GATCATGTTC TGGACCGACT GGGGAGACCT GAAGCCTGGG     2700
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TGGCCCAATG  GCATTTCCGT  GGACGATCAG  TGGATCTACT  GGACGGATGC  CTACCTGGAC      2820

TGCATTGAGC  GCATCACGTT  CAGCGGCCAG  CAGCGCTCCG  TCATCCTGGA  CAGACTCCCG      2880

CACCCCTATG  CCATTGCTGT  CTTTAAGAAT  GAGATTTACT  GGGATGACTG  GTCACAGCTC      2940

AGCATATTCC  GAGCTTCTAA  GTACAGCGGG  TCCCAGATGG  AGATTCTGGC  CAGCCAGCTC      3000

ACGGGGCTGA  TGGACATGAA  GATCTTCTAC  AAGGGGAAGA  ACACAGGAAG  CAATGCGTGT      3060

GTACCCAGGC  CGTGCAGCCT  GCTGTGCCTG  CCCAGAGCCA  ACAACAGCAA  AAGCTGCAGG      3120

TGTCCAGATG  GCGTGGCCAG  CAGTGTCCTC  CCTTCCGGGG  ACCTGATGTG  TGACTGCCCT      3180

AAGGGCTACG  AGCTGAAGAA  CAACACGTGT  GTCAAAGAAG  AAGACACCTG  TCTGCGCAAC      3240

CAGTACCGCT  GCAGCAACGG  GAACTGCATC  AACAGCATCT  GGTGGTGCGA  TTTCGACAAC      3300

GACTGCGGAG  ACATGAGCGA  CGAGAAGAAC  TGCCCTACCA  CCATCTGCGA  CCTGGACACC      3360

CAGTTCCGTT  GCCAGGAGTC  TGGGACGTGC  ATCCCGCTCT  CCTACAAATG  TGACCTCGAG      3420

GATGACTGTG  GGACAACAG   TGACGAAAGG  CACTGTGAAA  TGCACCAGTG  CCGGAGCGAC      3480

GAATACAACT  GCAGCTCGGG  CATGTGCATC  CGCTCCTCCT  GGGTGTGCGA  CGGGGACAAC      3540

GACTGCAGGG  ACTGGTCCGA  CGAGGCCAAC  TGCACAGCCA  TCTATCACAC  CTGTGAGGCC      3600

TCCAACTTCC  AGTGCCGCAA  CGGGCACTGC  ATCCCCCAGC  GGTGGGCGTG  TGACGGCGAC      3660

GCCGACTGCC  AGGATGGCTC  TGATGAGGAT  CCAGCCAACT  GTGAGAAGAA  GTGCAACGGC      3720

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TGCTCGGACG  GCTCCGACGA  GCAGCACTGC  GAGCCCCTGT  GTACACGGTT  CATGGACTTC      3840

GTGTGTAAGA  ACCGCCAGCA  GTGCCTCTTC  CACTCCATGG  TGTGCGATGG  GATCATCCAG      3900

TGCCGTGACG  GCTCCGACGA  GGACCCAGCC  TTTGCAGGAT  GCTCCCGAGA  CCCCGAGTTC      3960

CACAAGGTGT  GCGATGAGTT  CGGCTTCCAG  TGTCAGAACG  GCGTGTGCAT  CAGCTTGATC      4020

TGGAAGTGCG  ACGGGATGGA  TGACTGCGGG  GACTACTCCG  ACGAGGCCAA  CTGTGAAAAC      4080

CCCACAGAAG  CCCCCAACTG  CTCCCGCTAC  TTCCAGTTCC  GGTGTGACAA  TGGCCACTGC      4140

ATCCCCAACA  GGTGGAAGTG  TGACAGGGAG  AATGACTGTG  GGGACTGGTC  CGACGAGAAG      4200

GACTGTGGAG  ATTCACATGT  ACTTCCGTCT  ACGACTCCTG  CACCCTCCAC  GTGTCTGCCC      4260

AATTACTACC  GCTGCGGCGG  GGGGGCCTGC  GTGATAGACA  CGTGGGTTTG  TGACGGGTAC      4320

CGAGATTGCG  CAGATGGATC  CGACGAGGAA  GCCTGCCCCT  CGCTCCCCAA  TGTCACTGCC      4380

ACCTCCTCCC  CCTCCCAGCC  TGGACGATGC  GACCGATTTG  AGTTTGAGTG  CCACCAGCCA      4440

AAGAAGTGCA  TCCCTAACTG  GAGACGCTGT  GACGGCCATC  AGGATTGCCA  GGATGGCCAG      4500

GACGAGGCCA  ACTGCCCCAC  TCACAGCACC  TTGACCTGCA  TGAGCTGGGA  GTTCAAGTGT      4560

GAGGATGGCG  AGGCCTGCAT  CGTGCTGTCA  GAACGCTGCG  ACGGCTTCCT  GGACTGCTCA      4620
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GATGAGAGCG ACGAGAAGGC CTGCAGTGAT GAGTTAACTG TATACAAAGT ACAGAATCTT    4680

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CCCTCTGCTG CTTGTGTATA CAACGTGTAC TATAGAGTTG TTGGAGAGAG CATATGGAAG    4800

ACTCTGGAGA CTCACAGCAA TAAGACAAAC ACTGTATTAA AAGTGTTGAA ACCAGATACC    4860

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CACGGGGAAG AGGAAGGTGT GATTGTGGGC CACTGGAGCC CTCCCACCCA CACCCACGGC    5040

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TCCCTGAGTT TTACCCTGAC CGTGGATGGG AACATCAAGG TGAATGGCTA TGTGGTGAAC    5340

CTTTTCTGGG CATTTGACAC CCACAAACAA GAGAAGAAAA CCATGAACTT CCAAGGGAGC    5400

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GCCAAGACTG ACTTGGGCGA TAGTCCTCTG TCATTTGAGC ATGTCACGAC CAGAGGGGTT    5520

CGCCCACCTG CTCCTAGCCT CAAGGCCAGG GCTATCAATC AGACTGCAGT GGAATGCACC    5580

TGGACAGGCC CCAGGAATGT GGTGTATGGC ATTTTCTATG CCACATCCTT CCTGGACCTC    5640

TACCGCAACC CAAGCAGCCT GACCACGCCG CTGCACAACG CAACCGTGCT CGTCGGTAAG    5700

GATGAGCAGT ATCTGTTTCT GGTCCGGGTG GTGATGCCCT ACCAAGGGCC GTCCTCGGAC    5760

TACGTGGTCG TGAAGATGAT CCCGGACAGC AGGCTTCCTC CCCGGCACCT GCATGCCGTT    5820

CACACCGGCA AGACCTCGGC CGTCATCAAG TGGGAGTCGC CCTACGACTC TCCTGACCAG    5880

GACCTGTTCT ATGCGATCGC AGTTAAAGAT CTGATACGAA AGACGGACCG GAGCTACAAA    5940

GTCAAGTCCC GCAACAGCAC CGTGGAGTAC ACCCTGAGCA AGCTGGAGCC CGGAGGGAAA    6000

TACCACGTCA TTGTGCAGCT GGGGAACATG AGCAAAGATG CCAGTGTGAA GATCACCACC    6060

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TTCTGGAAAA GTCTAGCTCT AAAGGAAAAG TATTTTAACG AAAGCAGGGG CTACGAGATA    6180

CACATGTTTG ATAGCGCCAT GAATATCACC GCATACCTTG GAATACTAC  TGACAATTTC    6240

TTTAAAATTT CCAACCTGAA GATGGGTCAC AATTACACAT TCACGGTCCA GGCACGATGC    6300

CTTTTGGGCA GCCAGATCTG CGGGGAGCCT GCCGTGCTAC TGTATGATGA GCTGGGGTCT    6360

GGTGGCGATG CGTCGGCGAT GCAGGCTGCC AGGTCTACTG ATGTCGCCGC CGTGGTGGTG    6420

CCCATCCTGT TTCTGATACT GCTGAGCCTG GGGGTCGGGT TTGCCATCCT GTACACGAAG    6480

CATCGGAGGC TGCAGAGCAG CTTCACCGCC TTCGCCAACA GCCACTACAG CTCCAGACTC    6540
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GGCTCCGCCA TCTTCTCCTC TGGGGATGAC TTGGGGGAGG ATGATGAAGA TGCTCCTATG 6600

ATCACTGGAT TTTCGGACGA CGTCCCCATG GTGATAGCC 6639

(2) INFORMATION FOR SEQ ID NO: 2:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 2213 amino acids
       (B) TYPE: amino acid
       (C) STRANDEDNESS:
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Met Ala Thr Arg Ser Ser Arg Arg Glu Ser Arg Leu Pro Phe Leu Phe
1               5                   10                  15

Thr Leu Val Ala Leu Leu Pro Pro Gly Ala Leu Cys Glu Val Trp Thr
            20                  25                  30

Arg Thr Leu His Gly Gly Arg Ala Pro Leu Pro Gln Glu Arg Gly Phe
        35                  40                  45

Arg Val Val Gln Gly Asp Pro Arg Glu Leu Arg Leu Trp Glu Arg Gly
    50                  55                  60

Asp Ala Arg Gly Ala Ser Arg Ala Asp Glu Lys Pro Leu Arg Arg Arg
65                  70                  75                  80

Arg Ser Ala Ala Leu Gln Pro Glu Pro Ile Lys Val Tyr Gly Gln Val
                85                  90                  95

Ser Leu Asn Asp Ser His Asn Gln Met Val Val His Trp Ala Gly Glu
            100                 105                 110

Lys Ser Asn Val Ile Val Ala Leu Ala Arg Asp Ser Leu Ala Leu Ala
        115                 120                 125

Arg Pro Arg Ser Ser Asp Val Tyr Val Ser Tyr Asp Tyr Gly Lys Ser
    130                 135                 140

Phe Asn Lys Ile Ser Glu Lys Leu Asn Phe Gly Ala Gly Asn Asn Thr
145                 150                 155                 160

Glu Ala Val Val Ala Gln Phe Tyr His Ser Pro Ala Asp Asn Lys Arg
                165                 170                 175

Tyr Ile Phe Ala Asp Ala Tyr Ala Gln Tyr Leu Trp Ile Thr Phe Asp
            180                 185                 190

Phe Cys Asn Thr Ile His Gly Phe Ser Ile Pro Phe Arg Ala Ala Asp
        195                 200                 205

Leu Leu Leu His Ser Lys Ala Ser Asn Leu Leu Leu Gly Phe Asp Arg
    210                 215                 220

Ser His Pro Asn Lys Gln Leu Trp Lys Ser Asp Asp Phe Gly Gln Thr
225                 230                 235                 240
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Trp Ile Met Ile Gln Glu His Val Lys Ser Phe Ser Trp Gly Ile Asp
             245             250             255

Pro Tyr Asp Lys Pro Asn Thr Ile Tyr Ile Glu Arg His Glu Pro Ser
             260             265             270

Gly Tyr Ser Thr Val Phe Arg Ser Thr Asp Phe Phe Gln Ser Arg Glu
             275             280             285

Asn Gln Glu Val Ile Leu Glu Glu Val Arg Asp Phe Gln Leu Arg Asp
    290             295             300

Lys Tyr Met Phe Ala Thr Lys Val Val His Leu Leu Gly Ser Pro Leu
305             310             315             320

Gln Ser Ser Val Gln Leu Trp Val Ser Phe Gly Arg Lys Pro Met Arg
             325             330             335

Ala Ala Gln Phe Val Thr Arg His Pro Ile Asn Glu Tyr Tyr Ile Ala
             340             345             350

Asp Ala Ser Glu Asp Gln Val Phe Val Cys Val Ser His Ser Asn Asn
             355             360             365

Arg Thr Asn Leu Tyr Ile Ser Glu Ala Glu Gly Leu Lys Phe Ser Leu
    370             375             380

Ser Leu Glu Asn Val Leu Tyr Tyr Thr Pro Gly Gly Ala Gly Ser Asp
385             390             395             400

Thr Leu Val Arg Tyr Phe Ala Asn Glu Pro Phe Ala Asp Phe His Arg
             405             410             415

Val Glu Gly Leu Gln Gly Val Tyr Ile Ala Thr Leu Ile Asn Gly Ser
             420             425             430

Met Asn Glu Glu Asn Met Arg Ser Val Ile Thr Phe Asp Lys Gly Gly
    435             440             445

Thr Trp Glu Phe Leu Gln Ala Pro Ala Phe Thr Gly Tyr Gly Glu Lys
    450             455             460

Ile Asn Cys Glu Leu Ser Glu Gly Cys Ser Leu His Leu Ala Gln Arg
465             470             475             480

Leu Ser Gln Leu Leu Asn Leu Gln Leu Arg Arg Met Pro Ile Leu Ser
             485             490             495

Lys Glu Ser Ala Pro Gly Leu Ile Ile Ala Thr Gly Ser Val Gly Lys
             500             505             510

Asn Leu Ala Ser Lys Thr Asn Val Tyr Ile Ser Ser Ser Ala Gly Ala
             515             520             525

Arg Trp Arg Glu Ala Leu Pro Gly Pro His Tyr Tyr Thr Trp Gly Asp
             530             535             540

His Gly Gly Ile Ile Met Ala Ile Ala Gln Gly Met Glu Thr Asn Glu
545             550             555             560

Leu Lys Tyr Ser Thr Asn Glu Gly Glu Thr Trp Lys Ala Phe Thr Phe
             565             570             575
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Ser Glu Lys Pro Val Phe Val Tyr Gly Leu Leu Thr Glu Pro Gly Glu
             580             585             590

Lys Ser Thr Val Phe Thr Ile Phe Gly Ser Asn Lys Glu Asn Val His
         595             600             605

Ser Trp Leu Ile Leu Gln Val Asn Ala Thr Asp Ala Leu Gly Val Pro
    610             615             620

Cys Thr Glu Asn Asp Tyr Lys Leu Trp Ser Pro Ser Asp Glu Arg Gly
625             630             635             640

Asn Glu Cys Leu Leu Gly His Lys Thr Val Phe Lys Arg Arg Thr Pro
             645             650             655

His Ala Thr Cys Phe Asn Gly Glu Asp Phe Asp Arg Pro Val Val Val
         660             665             670

Ser Asn Cys Ser Cys Thr Arg Glu Asp Tyr Glu Cys Asp Phe Gly Phe
    675             680             685

Arg Met Ser Glu Asp Leu Ala Leu Glu Val Cys Val Pro Asp Pro Gly
    690             695             700

Phe Ser Gly Lys Ser Ser Pro Pro Val Pro Cys Pro Val Gly Ser Thr
705             710             715             720

Tyr Arg Arg Ser Arg Gly Tyr Arg Lys Ile Ser Gly Asp Thr Cys Ser
             725             730             735

Gly Gly Asp Val Glu Ala Arg Leu Glu Gly Glu Leu Val Pro Cys Pro
         740             745             750

Leu Ala Glu Glu Asn Glu Phe Ile Leu Tyr Ala Thr Arg Lys Ser Ile
    755             760             765

His Arg Tyr Asp Leu Ala Ser Gly Thr Thr Glu Gln Leu Pro Leu Thr
    770             775             780

Gly Leu Arg Ala Ala Val Ala Leu Asp Phe Asp Tyr Glu His Asn Cys
785             790             795             800

Leu Tyr Trp Ser Asp Leu Ala Leu Asp Val Ile Gln Arg Leu Cys Leu
             805             810             815

Asn Gly Ser Thr Gly Gln Glu Val Ile Ile Asn Ser Asp Leu Glu Thr
             820             825             830

Val Glu Ala Leu Ala Phe Glu Pro Leu Ser Gln Leu Leu Tyr Trp Val
         835             840             845

Asp Ala Gly Phe Lys Lys Ile Glu Val Ala Asn Pro Asp Gly Asp Phe
    850             855             860

Arg Leu Thr Val Val Asn Ser Ser Val Leu Asp Arg Pro Arg Ala Leu
865             870             875             880

Val Leu Val Pro Gln Glu Gly Ile Met Phe Trp Thr Asp Trp Gly Asp
             885             890             895

Leu Lys Pro Gly Ile Tyr Arg Ser Asn Met Asp Gly Ser Ala Ala Tyr
             900             905             910

Arg Leu Val Ser Glu Asp Val Lys Trp Pro Asn Gly Ile Ser Val Asp
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                      915                        920                        925
        Asp Gln Trp Ile Tyr Trp Thr Asp Ala Tyr Leu Asp Cys Ile Glu Arg
            930                     935                    940
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        Ile Thr Phe Ser Gly Gln Gln Arg Ser Val Ile Leu Asp Arg Leu Pro
        945             950                 955                        960

        His Pro Tyr Ala Ile Ala Val Phe Lys Asn Glu Ile Tyr Trp Asp Asp
10                      965             970                        975

        Trp Ser Gln Leu Ser Ile Phe Arg Ala Ser Lys Tyr Ser Gly Ser Gln
                    980             985                 990

        Met Glu Ile Leu Ala Ser Gln Leu Thr Gly Leu Met Asp Met Lys Ile
                    995             1000                1005
15
        Phe Tyr Lys Gly Lys Asn Thr Gly Ser Asn Ala Cys Val Pro Arg Pro
            1010                1015                1020

        Cys Ser Leu Leu Cys Leu Pro Arg Ala Asn Asn Ser Lys Ser Cys Arg
        1025                1030                1035                1040
20
        Cys Pro Asp Gly Val Ala Ser Ser Val Leu Pro Ser Gly Asp Leu Met
                    1045                1050                1055

        Cys Asp Cys Pro Lys Gly Tyr Glu Leu Lys Asn Asn Thr Cys Val Lys
                    1060            1065                1070

25      Glu Glu Asp Thr Cys Leu Arg Asn Gln Tyr Arg Cys Ser Asn Gly Asn
                    1075            1080                1085

        Cys Ile Asn Ser Ile Trp Trp Cys Asp Phe Asp Asn Asp Cys Gly Asp
            1090            1095                1100

30      Met Ser Asp Glu Lys Asn Cys Pro Thr Thr Ile Cys Asp Leu Asp Thr
        1105                1110                1115                1120

        Gln Phe Arg Cys Gln Glu Ser Gly Thr Cys Ile Pro Leu Ser Tyr Lys
                    1125                1130                1135

35      Cys Asp Leu Glu Asp Asp Cys Gly Asp Asn Ser Asp Glu Arg His Cys
                1140                1145                1150

        Glu Met His Gln Cys Arg Ser Asp Glu Tyr Asn Cys Ser Ser Gly Met
                1155                1160                1165

40      Cys Ile Arg Ser Ser Trp Val Cys Asp Gly Asp Asn Asp Cys Arg Asp
            1170            1175                1180

        Trp Ser Asp Glu Ala Asn Cys Thr Ala Ile Tyr His Thr Cys Glu Ala
        1185                1190                1195                1200

45      Ser Asn Phe Gln Cys Arg Asn Gly His Cys Ile Pro Gln Arg Trp Ala
                        1205                1210                1215

        Cys Asp Gly Asp Ala Asp Cys Gln Asp Gly Ser Asp Glu Asp Pro Ala
                    1220                1225                1230

50      Asn Cys Glu Lys Lys Cys Asn Gly Phe Arg Cys Pro Asn Gly Thr Cys
                1235                1240                1245

        Ile Pro Ser Thr Lys His Cys Asp Gly Leu His Asp Cys Ser Asp Gly
            1250                1255                1260

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Ser Asp Glu Gln His Cys Glu Pro Leu Cys Thr Arg Phe Met Asp Phe
1265   1270   1275   Phe Met Asp 1280

Val Cys Lys Asn Arg Gln Gln Cys Leu Phe His Ser Met Val Cys Asp
                1285   1290   1295

Gly Ile Ile Gln Cys Arg Asp Gly Ser Asp Glu Asp Pro Ala Phe Ala
                1300   1305   1310

Gly Cys Ser Arg Asp Pro Glu Phe His Lys Val Cys Asp Glu Phe Gly
                1315   1320   1325

Phe Gln Cys Gln Asn Gly Val Cys Ile Ser Leu Ile Trp Lys Cys Asp
                1330   1335   1340

Gly Met Asp Asp Cys Gly Asp Tyr Ser Asp Glu Ala Asn Cys Glu Asn
1345   1350   1355   1360

Pro Thr Glu Ala Pro Asn Cys Ser Arg Tyr Phe Gln Phe Arg Cys Asp
                1365   1370   1375

Asn Gly His Cys Ile Pro Asn Arg Trp Lys Cys Asp Arg Glu Asn Asp
                1380   1385   1390

Cys Gly Asp Trp Ser Asp Glu Lys Asp Cys Gly Asp Ser His Val Leu
                1395   1400   1405

Pro Ser Thr Thr Pro Ala Pro Ser Thr Cys Leu Pro Asn Tyr Tyr Arg
                1410   1415   1420

Cys Gly Gly Gly Ala Cys Val Ile Asp Thr Trp Val Cys Asp Gly Tyr
1425   1430   1435   1440

Arg Asp Cys Ala Asp Gly Ser Asp Glu Glu Ala Cys Pro Ser Leu Pro
                1445   1450   1455

Asn Val Thr Ala Thr Ser Ser Pro Ser Gln Pro Gly Arg Cys Asp Arg
                1460   1465   1470

Phe Glu Phe Glu Cys His Gln Pro Lys Lys Cys Ile Pro Asn Trp Arg
                1475   1480   1485

Arg Cys Asp Gly His Gln Asp Cys Gln Asp Gly Gln Asp Glu Ala Asn
                1490   1495   1500

Cys Pro Thr His Ser Thr Leu Thr Cys Met Ser Trp Glu Phe Lys Cys
1505   1510   1515   1520

Glu Asp Gly Glu Ala Cys Ile Val Leu Ser Glu Arg Cys Asp Gly Phe
                1525   1530   1535

Leu Asp Cys Ser Asp Glu Ser Asp Glu Lys Ala Cys Ser Asp Glu Leu
                1540   1545   1550

Thr Val Tyr Lys Val Gln Asn Leu Gln Trp Thr Ala Asp Phe Ser Gly
                1555   1560   1565

Asn Val Thr Leu Thr Trp Met Arg Pro Lys Lys Met Pro Ser Ala Ala
                1570   1575   1580

Cys Val Tyr Asn Val Tyr Tyr Arg Val Val Gly Glu Ser Ile Trp Lys
1585   1590   1595   1600

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Thr Leu Glu Thr His Ser Asn Lys Thr Asn Thr Val Leu Lys Val Leu
            1605                1610              1615

Lys Pro Asp Thr Thr Tyr Gln Val Lys Val Gln Val Gln Cys Leu Ser
            1620            1625                1630

Lys Val His Asn Thr Asn Asp Phe Val Thr Leu Arg Thr Pro Glu Gly
        1635                1640              1645

Leu Pro Asp Ala Pro Gln Asn Leu Gln Leu Ser Leu His Gly Glu Glu
        1650                1655                1660

Glu Gly Val Ile Val Gly His Trp Ser Pro Pro Thr His Thr His Gly
1665              1670              1675                    1680

Leu Ile Arg Glu Tyr Ile Val Glu Tyr Ser Arg Ser Gly Ser Lys Val
                1685                1690                1695

Trp Thr Ser Glu Arg Ala Ala Ser Asn Phe Thr Glu Ile Lys Asn Leu
            1700                1705                1710

Leu Val Asn Thr Leu Tyr Thr Val Arg Val Ala Ala Val Thr Ser Arg
            1715                1720                1725

Gly Ile Gly Asn Trp Ser Asp Ser Lys Ser Ile Thr Thr Val Lys Gly
    1730                1735                1740

Lys Ala Ile Pro Pro Pro Asn Ile His Ile Asp Asn Tyr Asp Glu Asn
1745                1750                1755                    1760

Ser Leu Ser Phe Thr Leu Thr Val Asp Gly Asn Ile Lys Val Asn Gly
                1765                1770                1775

Tyr Val Val Asn Leu Phe Trp Ala Phe Asp Thr His Lys Gln Glu Lys
            1780                1785                1790

Lys Thr Met Asn Phe Gln Gly Ser Ser Val Ser His Lys Val Gly Asn
            1795                1800                1805

Leu Thr Ala Gln Thr Ala Tyr Glu Ile Ser Ala Trp Ala Lys Thr Asp
        1810                1815                1820

Leu Gly Asp Ser Pro Leu Ser Phe Glu His Val Thr Thr Arg Gly Val
1825                1830                1835                    1840

Arg Pro Pro Ala Pro Ser Leu Lys Ala Arg Ala Ile Asn Gln Thr Ala
            1845                1850                1855

Val Glu Cys Thr Trp Thr Gly Pro Arg Asn Val Val Tyr Gly Ile Phe
            1860                1865                1870

Tyr Ala Thr Ser Phe Leu Asp Leu Tyr Arg Asn Pro Ser Ser Leu Thr
        1875                1880                1885

Thr Pro Leu His Asn Ala Thr Val Leu Val Gly Lys Asp Glu Gln Tyr
    1890                1895                1900

Leu Phe Leu Val Arg Val Val Met Pro Tyr Gln Gly Pro Ser Ser Asp
1905                1910                1915                    1920

Tyr Val Val Val Lys Met Ile Pro Asp Ser Arg Leu Pro Pro Arg His
                1925                1930                1935

Leu His Ala Val His Thr Gly Lys Thr Ser Ala Val Ile Lys Trp Glu
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                  1940                    1945                    1950
        Ser Pro Tyr Asp Ser Pro Asp Gln Asp Leu Phe Tyr Ala Ile Ala Val
                    1955                1960                1965
        Lys Asp Leu Ile Arg Lys Thr Asp Arg Ser Tyr Lys Val Lys Ser Arg
              1970                1975                1980
        Asn Ser Thr Val Glu Tyr Thr Leu Ser Lys Leu Glu Pro Gly Gly Lys
              1985                1990             1995                2000
        Tyr His Val Ile Val Gln Leu Gly Asn Met Ser Lys Asp Ala Ser Val
                    2005                2010                2015
        Lys Ile Thr Thr Val Ser Leu Ser Ala Pro Asp Ala Leu Lys Ile Ile
                    2020                2025                2030
        Thr Glu Asn Asp His Val Leu Leu Phe Trp Lys Ser Leu Ala Leu Lys
                    2035                2040                2045
        Glu Lys Tyr Phe Asn Glu Ser Arg Gly Tyr Glu Ile His Met Phe Asp
              2050                2055                2060
        Ser Ala Met Asn Ile Thr Ala Tyr Leu Gly Asn Thr Thr Asp Asn Phe
        2065                2070                2075                2080
        Phe Lys Ile Ser Asn Leu Lys Met Gly His Asn Tyr Thr Phe Thr Val
                    2085                2090                2095
        Gln Ala Arg Cys Leu Leu Gly Ser Gln Ile Cys Gly Glu Pro Ala Val
                    2100                2105                2110
        Leu Leu Tyr Asp Glu Leu Gly Ser Gly Gly Asp Ala Ser Ala Met Gln
                    2115                2120                2125
        Ala Ala Arg Ser Thr Asp Val Ala Ala Val Val Val Pro Ile Leu Phe
                    2130                2135                2140
        Leu Ile Leu Leu Ser Leu Gly Val Gly Phe Ala Ile Leu Tyr Thr Lys
        2145                2150                2155                2160
        His Arg Arg Leu Gln Ser Ser Phe Thr Ala Phe Ala Asn Ser His Tyr
                    2165                2170                2175
        Ser Ser Arg Leu Gly Ser Ala Ile Phe Ser Ser Gly Asp Asp Leu Gly
                    2180                2185                2190
        Glu Asp Asp Glu Asp Ala Pro Met Ile Thr Gly Phe Ser Asp Asp Val
                    2195                2200                2205
        Pro Met Val Ile Ala
              2210
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(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6961 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:
    (A) NAME/KEY: sig peptide
    (B) LOCATION:178..261

(ix) FEATURE:
    (A) NAME/KEY: mat peptide
    (B) LOCATION:262..6816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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CCGCGAGCCG CACACGTGAC GGCGCCGCGC CGCGCCGCGC CGCGCCGAGC GGGACCCAGC   60
GGCTGCCCGG AGCCCCGGGA GCGGCGCGCG CGCGGCCCCG GCCCCGCCGC TCGGCCGGCG  120
GCGCGCTGCA CATTCTCTCC TGGCGGCGGC GCCACCTGCA GCCGCGTTCG CCCGAACATG  180
                                                               Met
                                                                 1

GCG ACA CGG AGC AGC AGG AGG GAG TCG CGA CTC CCC TTC CTA TTC ACC   228
Ala Thr Arg Ser Ser Arg Arg Glu Ser Arg Leu Pro Phe Leu Phe Thr
            5                  10                  15

CTG GTC GCG CTG CTG CCG CCC GGG GCT CTC TGC GAG GTG TGG ACG CGG   276
Leu Val Ala Leu Leu Pro Pro Gly Ala Leu Cys Glu Val Trp Thr Arg
        20                  25                  30

ACA CTG CAC GGC GGC CGC GCG CCC TTA CCC CAG GAG CGG GGC TTC CGC   324
Thr Leu His Gly Gly Arg Ala Pro Leu Pro Gln Glu Arg Gly Phe Arg
    35                  40                  45

GTG GTG CAG GGC GAC CCG CGC GAG CTG CGG CTG TGG GAG CGC GGG GAT   372
Val Val Gln Gly Asp Pro Arg Glu Leu Arg Leu Trp Glu Arg Gly Asp
50                  55                  60                  65

GCC AGG GGG GCG AGC CGG GCG GAC GAG AAG CCG CTC CGG AGG AGA CGG   420
Ala Arg Gly Ala Ser Arg Ala Asp Glu Lys Pro Leu Arg Arg Arg Arg
            70                  75                  80

AGC GCT GCC CTG CAG CCC GAG CCC ATC AAG GTG TAC GGA CAG GTC AGC   468
Ser Ala Ala Leu Gln Pro Glu Pro Ile Lys Val Tyr Gly Gln Val Ser
            85                  90                  95

CTC AAT GAT TCC CAC AAT CAG ATG GTG GTG CAC TGG GCC GGA GAG AAA   516
Leu Asn Asp Ser His Asn Gln Met Val Val His Trp Ala Gly Glu Lys
        100                 105                 110

AGC AAC GTG ATC GTG GCC TTG GCC CGG GAC AGC CTG GCG TTG GCC AGG   564
Ser Asn Val Ile Val Ala Leu Ala Arg Asp Ser Leu Ala Leu Ala Arg
    115                 120                 125

CCC AGG AGC AGT GAT GTG TAC GTG TCT TAT GAC TAT GGA AAA TCA TTC   612
Pro Arg Ser Ser Asp Val Tyr Val Ser Tyr Asp Tyr Gly Lys Ser Phe
130                 135                 140                 145

AAT AAG ATT TCA GAG AAA TTG AAC TTC GGC GCG GGA AAT AAC ACA GAG   660
Asn Lys Ile Ser Glu Lys Leu Asn Phe Gly Ala Gly Asn Asn Thr Glu
                150                 155                 160

GCT GTG GTG GCC CAG TTC TAC CAC AGC CCT GCG GAC AAC AAA CGG TAC   708
Ala Val Val Ala Gln Phe Tyr His Ser Pro Ala Asp Asn Lys Arg Tyr
            165                 170                 175

ATC TTC GCA GAT GCC TAC GCC CAG TAT CTC TGG ATC ACG TTT GAC TTC   756
Ile Phe Ala Asp Ala Tyr Ala Gln Tyr Leu Trp Ile Thr Phe Asp Phe
        180                 185                 190

TGC AAC ACC ATC CAT GGC TTT TCC ATC CCG TTC CGG GCA GCT GAT CTC   804
Cys Asn Thr Ile His Gly Phe Ser Ile Pro Phe Arg Ala Ala Asp Leu
    195                 200                 205

CTA CTC CAC AGT AAG GCC TCC AAC CTT CTC CTG GGC TTC GAC AGG TCT   852
Leu Leu His Ser Lys Ala Ser Asn Leu Leu Leu Gly Phe Asp Arg Ser
210                 215                 220                 225

CAC CCC AAC AAG CAG CTG TGG AAG TCG GAT GAT TTT GGC CAG ACC TGG   900
His Pro Asn Lys Gln Leu Trp Lys Ser Asp Asp Phe Gly Gln Thr Trp
                230                 235                 240

ATC ATG ATT CAA GAA CAC GTG AAG TCC TTT TCT TGG GGA ATT GAT CCC   948
Ile Met Ile Gln Glu His Val Lys Ser Phe Ser Trp Gly Ile Asp Pro
            245                 250                 255
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TAT GAC AAA CCA AAC ACC ATC TAC ATC GAA CGG CAC GAA CCT TCT GGC        996
Tyr Asp Lys Pro Asn Thr Ile Tyr Ile Glu Arg His Glu Pro Ser Gly
        260                 265                 270
TAC TCC ACG GTT TTC CGA AGT ACA GAC TTC TTC CAG TCC CGG GAA AAC       1044
Tyr Ser Thr Val Phe Arg Ser Thr Asp Phe Phe Gln Ser Arg Glu Asn
        275                 280                 285
CAG GAA GTG ATC TTG GAG GAA GTG AGA GAC TTT CAG CTT CGG GAC AAG       1092
Gln Glu Val Ile Leu Glu Glu Val Arg Asp Phe Gln Leu Arg Asp Lys
290                 295                 300                 305
TAC ATG TTT GCT ACA AAG GTG GTG CAT CTC TTG GGC AGT CCA CTG CAG       1140
Tyr Met Phe Ala Thr Lys Val Val His Leu Leu Gly Ser Pro Leu Gln
                310                 315                 320
TCT TCT GTC CAG CTC TGG GTC TCC TTT GGC CGG AAG CCC ATG CGG GCC       1188
Ser Ser Val Gln Leu Trp Val Ser Phe Gly Arg Lys Pro Met Arg Ala
                325                 330                 335
GCC CAG TTT GTT ACA AGA CAT CCT ATC AAC GAA TAT TAC ATC GCG GAT       1236
Ala Gln Phe Val Thr Arg His Pro Ile Asn Glu Tyr Tyr Ile Ala Asp
                340                 345                 350
GCC TCG GAG GAC CAG GTG TTT GTG TGT GTC AGT CAC AGC AAC AAC CGC       1284
Ala Ser Glu Asp Gln Val Phe Val Cys Val Ser His Ser Asn Asn Arg
        355                 360                 365
ACC AAC CTC TAC ATC TCG GAG GCA GAG GGC TTG AAG TTC TCT CTG TCC       1332
Thr Asn Leu Tyr Ile Ser Glu Ala Glu Gly Leu Lys Phe Ser Leu Ser
370                 375                 380                 385
CTG GAG AAC GTG CTC TAC TAC ACC CCG GGA GGG GCC GGC AGT GAC ACC       1380
Leu Glu Asn Val Leu Tyr Tyr Thr Pro Gly Gly Ala Gly Ser Asp Thr
                390                 395                 400
TTG GTG AGG TAC TTT GCA AAT GAA CCG TTT GCT GAC TTC CAT CGT GTG       1428
Leu Val Arg Tyr Phe Ala Asn Glu Pro Phe Ala Asp Phe His Arg Val
                405                 410                 415
GAA GGG TTG CAG GGA GTC TAC ATT GCT ACT CTG ATT AAT GGT TCT ATG       1476
Glu Gly Leu Gln Gly Val Tyr Ile Ala Thr Leu Ile Asn Gly Ser Met
                420                 425                 430
AAT GAG GAG AAC ATG AGA TCT GTC ATC ACC TTT GAC AAA GGG GGC ACC       1524
Asn Glu Glu Asn Met Arg Ser Val Ile Thr Phe Asp Lys Gly Gly Thr
        435                 440                 445
TGG GAA TTT CTG CAG GCT CCA GCC TTC ACG GGG TAT GGA GAG AAA ATC       1572
Trp Glu Phe Leu Gln Ala Pro Ala Phe Thr Gly Tyr Gly Glu Lys Ile
450                 455                 460                 465
AAC TGT GAG CTG TCC GAG GGC TGT TCC CTC CAC CTG GCC CAG CGC CTC       1620
Asn Cys Glu Leu Ser Glu Gly Cys Ser Leu His Leu Ala Gln Arg Leu
                470                 475                 480
AGC CAG CTG CTC AAC CTC CAG CTC CGG AGG ATG CCC ATC CTG TCC AAG       1668
Ser Gln Leu Leu Asn Leu Gln Leu Arg Arg Met Pro Ile Leu Ser Lys
                485                 490                 495
GAG TCG GCG CCT GGC CTC ATC ATT GCC ACG GGC TCA GTG GGA AAG AAC       1716
Glu Ser Ala Pro Gly Leu Ile Ile Ala Thr Gly Ser Val Gly Lys Asn
                500                 505                 510
TTG GCT AGC AAG ACA AAC GTG TAC ATC TCT AGC AGT GCT GGA GCC AGG       1764
Leu Ala Ser Lys Thr Asn Val Tyr Ile Ser Ser Ser Ala Gly Ala Arg
        515                 520                 525
TGG CGA GAG GCA CTT CCT GGA CCT CAC TAC TAT ACA TGG GGA GAC CAT       1812
Trp Arg Glu Ala Leu Pro Gly Pro His Tyr Tyr Thr Trp Gly Asp His
530                 535                 540                 545
GGC GGC ATC ATC ATG GCC ATT GCC CAA GGC ATG GAA ACC AAC GAA CTG       1860
Gly Gly Ile Ile Met Ala Ile Ala Gln Gly Met Glu Thr Asn Glu Leu
                550                 555                 560
AAG TAC AGT ACC AAC GAA GGG GAG ACC TGG AAA GCC TTC ACC TTC TCT       1908
Lys Tyr Ser Thr Asn Glu Gly Glu Thr Trp Lys Ala Phe Thr Phe Ser
                565                 570                 575
GAG AAG CCC GTG TTT GTG TAT GGG CTC CTC ACG GAA CCC GGC GAG AAG       1956
Glu Lys Pro Val Phe Val Tyr Gly Leu Leu Thr Glu Pro Gly Glu Lys
                580                 585                 590
AGC ACG GTC TTC ACC ATC TTT GGC TCC AAC AAG GAG AAC GTG CAC AGC       2004
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    Ser Thr Val Phe Thr Ile Phe Gly Ser Asn Lys Glu Asn Val His Ser
        595             600             605
    TGG CTC ATC CTC CAG GTC AAT GCC ACA GAC GCC CTG GGG GTT CCT TGC    2052
    Trp Leu Ile Leu Gln Val Asn Ala Thr Asp Ala Leu Gly Val Pro Cys
    610             615             620             625
    ACA GAG AAC GAC TAC AAG CTC TGG TCA CCA TCT GAT GAG CGG GGG AAT    2100
    Thr Glu Asn Asp Tyr Lys Leu Trp Ser Pro Ser Asp Glu Arg Gly Asn
                630             635             640
    GAG TGT TTG CTT GGA CAC AAG ACT GTT TTC AAA CGG AGG ACC CCG CAC    2148
    Glu Cys Leu Leu Gly His Lys Thr Val Phe Lys Arg Arg Thr Pro His
                645             650             655
    GCC ACA TGC TTT AAC GGA GAA GAC TTT GAC AGG CCG GTG GTT GTG TCC    2196
    Ala Thr Cys Phe Asn Gly Glu Asp Phe Asp Arg Pro Val Val Val Ser
                660             665             670
    AAC TGC TCC TGC ACC CGG GAG GAC TAT GAG TGT GAC TTT GGC TTC CGG    2244
    Asn Cys Ser Cys Thr Arg Glu Asp Tyr Glu Cys Asp Phe Gly Phe Arg
                675             680             685
    ATG AGT GAA GAC TTG GCA TTA GAG GTG TGT GTT CCA GAT CCA GGA TTT    2292
    Met Ser Glu Asp Leu Ala Leu Glu Val Cys Val Pro Asp Pro Gly Phe
    690             695             700             705
    TCT GGA AAG TCC TCC CCT CCA GTG CCT TGT CCC GTG GGC TCT ACG TAC    2340
    Ser Gly Lys Ser Ser Pro Pro Val Pro Cys Pro Val Gly Ser Thr Tyr
                710             715             720
    AGG CGA TCA AGA GGC TAC CGG AAG ATT TCT GGG GAC ACC TGT AGT GGA    2388
    Arg Arg Ser Arg Gly Tyr Arg Lys Ile Ser Gly Asp Thr Cys Ser Gly
                725             730             735
    GGA GAT GTT GAG GCA CGG CTA GAA GGA GAG CTG GTC CCC TGT CCC CTG    2436
    Gly Asp Val Glu Ala Arg Leu Glu Gly Glu Leu Val Pro Cys Pro Leu
                740             745             750
    GCA GAA GAG AAC GAG TTC ATC CTG TAC GCC ACG CGC AAG TCC ATC CAC    2484
    Ala Glu Glu Asn Glu Phe Ile Leu Tyr Ala Thr Arg Lys Ser Ile His
    755             760             765
    CGC TAT GAC CTG GCT TCC GGA ACC ACG GAG CAG TTG CCC CTC ACT GGG    2532
    Arg Tyr Asp Leu Ala Ser Gly Thr Thr Glu Gln Leu Pro Leu Thr Gly
    770             775             780             785
    TTG CGG GCA GCA GTG GCC CTG GAC TTT GAC TAT GAG CAC AAC TGC CTG    2580
    Leu Arg Ala Ala Val Ala Leu Asp Phe Asp Tyr Glu His Asn Cys Leu
                790             795             800
    TAT TGG TCT GAC CTG GCC TTG GAC GTC ATC CAG CGC CTC TGT TTG AAC    2628
    Tyr Trp Ser Asp Leu Ala Leu Asp Val Ile Gln Arg Leu Cys Leu Asn
                805             810             815
    GGG AGT ACA GGA CAA GAG GTG ATC ATC AAC TCT GAC CTG GAG ACG GTA    2676
    Gly Ser Thr Gly Gln Glu Val Ile Ile Asn Ser Asp Leu Glu Thr Val
                820             825             830
    GAA GCT TTG GCT TTT GAA CCC CTC AGC CAA TTA CTT TAC TGG GTG GAC    2724
    Glu Ala Leu Ala Phe Glu Pro Leu Ser Gln Leu Leu Tyr Trp Val Asp
    835             840             845
    GCA GGC TTT AAA AAG ATC GAG GTA GCC AAT CCA GAT GGT GAC TTC CGA    2772
    Ala Gly Phe Lys Lys Ile Glu Val Ala Asn Pro Asp Gly Asp Phe Arg
    850             855             860             865
    CTC ACC GTC GTC AAT TCC TCG GTG CTG GAT CGG CCC CGG GCC CTG GTC    2820
    Leu Thr Val Val Asn Ser Ser Val Leu Asp Arg Pro Arg Ala Leu Val
                870             875             880
    CTT GTG CCC CAA GAA GGG ATC ATG TTC TGG ACC GAC TGG GGA GAC CTG    2868
    Leu Val Pro Gln Glu Gly Ile Met Phe Trp Thr Asp Trp Gly Asp Leu
                885             890             895
    AAG CCT GGG ATT TAT CGG AGC AAC ATG GAC GGA TCT GCC GCC TAT CGC    2916
    Lys Pro Gly Ile Tyr Arg Ser Asn Met Asp Gly Ser Ala Ala Tyr Arg
                900             905             910
    CTC GTG TCG GAG GAT GTG AAG TGG CCC AAT GGC ATT TCC GTG GAC GAT    2964
    Leu Val Ser Glu Asp Val Lys Trp Pro Asn Gly Ile Ser Val Asp Asp
    915             920             925
    CAG TGG ATC TAC TGG ACG GAT GCC TAC CTG GAC TGC ATT GAG CGC ATC    3012
    Gln Trp Ile Tyr Trp Thr Asp Ala Tyr Leu Asp Cys Ile Glu Arg Ile
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        930                    935                    940                    945
    ACG TTC AGC GGC CAG CAG CGC TCC GTC ATC CTG GAC ACA CTC CCG CAC
    Thr Phe Ser Gly Gln Gln Arg Ser Val Ile Leu Asp Arg Leu Pro His      3060
                        950                    955                    960
    CCC TAT GCC ATT GCT GTC TTT AAG AAT GAG ATT TAC TGG GAT GAC TGG
    Pro Tyr Ala Ile Ala Val Phe Lys Asn Glu Ile Tyr Trp Asp Asp Trp      3108
                        965                    970                    975
    TCA CAG CTC AGC ATA TTC CGA GCT TCT AAG TAC AGC GGG TCC CAG ATG
    Ser Gln Leu Ser Ile Phe Arg Ala Ser Lys Tyr Ser Gly Ser Gln Met      3156
                        980                    985                    990
    GAG ATT CTG GCC AGC CAG CTC ACG GGG CTG ATG GAC ATG AAG ATC TTC
    Glu Ile Leu Ala Ser Gln Leu Thr Gly Leu Met Asp Met Lys Ile Phe      3204
            995                    1000                   1005
    TAC AAG GGG AAG AAC ACA GGA AGC AAT GCG TGT GTA CCC AGG CCG TGC
    Tyr Lys Gly Lys Asn Thr Gly Ser Asn Ala Cys Val Pro Arg Pro Cys      3252
    1010                   1015                   1020                   1025
    AGC CTG CTG TGC CTG CCC AGA GCC AAC AAC AGC AAA AGC TGC AGG TGT
    Ser Leu Leu Cys Leu Pro Arg Ala Asn Asn Ser Lys Ser Cys Arg Cys      3300
                        1030                   1035                   1040
    CCA GAT GGC GTG GCC AGC AGT GTC CTC CCT TCC GGG GAC CTG ATG TGT
    Pro Asp Gly Val Ala Ser Ser Val Leu Pro Ser Gly Asp Leu Met Cys      3348
                        1045                   1050                   1055
    GAC TGC CCT AAG GGC TAC GAG CTG AAG AAC AAC ACG TGT GTC AAA GAA
    Asp Cys Pro Lys Gly Tyr Glu Leu Lys Asn Asn Thr Cys Val Lys Glu      3396
                1060                   1065                   1070
    GAA GAC ACC TGT CTG CGC AAC CAG TAC CGC TGC AGC AAC GGG AAC TGC
    Glu Asp Thr Cys Leu Arg Asn Gln Tyr Arg Cys Ser Asn Gly Asn Cys      3444
                1075                   1080                   1085
    ATC AAC AGC ATC TGG TGG TGC GAT TTC GAC AAC GAC TGC GGA GAC ATG
    Ile Asn Ser Ile Trp Trp Cys Asp Phe Asp Asn Asp Cys Gly Asp Met      3492
    1090                   1095                   1100                   1105
    AGC GAC GAG AAG AAC TGC CCT ACC ACC ATC TGC GAC CTG GAC ACC CAG
    Ser Asp Glu Lys Asn Cys Pro Thr Thr Ile Cys Asp Leu Asp Thr Gln      3540
                        1110                   1115                   1120
    TTC CGT TGC CAG GAG TCT GGG ACG TGC ATC CCG CTC TCC TAC AAA TGT
    Phe Arg Cys Gln Glu Ser Gly Thr Cys Ile Pro Leu Ser Tyr Lys Cys      3588
                        1125                   1130                   1135
    GAC CTC GAG GAT GAC TGT GGG GAC AAC AGT GAC GAA AGG CAC TGT GAA
    Asp Leu Glu Asp Asp Cys Gly Asp Asn Ser Asp Glu Arg His Cys Glu      3636
                        1140                   1145                   1150
    ATG CAC CAG TGC CGG AGC GAC GAA TAC AAC TGC AGC TCG GGC ATG TGC
    Met His Gln Cys Arg Ser Asp Glu Tyr Asn Cys Ser Ser Gly Met Cys      3684
                1155                   1160                   1165
    ATC CGC TCC TCC TGG GTG TGC GAC GGG GAC AAC GAC TGC AGG GAC TGG
    Ile Arg Ser Ser Trp Val Cys Asp Gly Asp Asn Asp Cys Arg Asp Trp      3732
    1170                   1175                   1180                   1185
    TCC GAC GAG GCC AAC TGC ACA GCC ATC TAT CAC ACC TGT GAG GCC TCC
    Ser Asp Glu Ala Asn Cys Thr Ala Ile Tyr His Thr Cys Glu Ala Ser      3780
                        1190                   1195                   1200
    AAC TTC CAG TGC CGC AAC GGG CAC TGC ATC CCC CAG CGG TGG GCG TGT
    Asn Phe Gln Cys Arg Asn Gly His Cys Ile Pro Gln Arg Trp Ala Cys      3828
                        1205                   1210                   1215
    GAC GGC GAC GCC GAC TGC CAG GAT GGC TCT GAT GAG GAT CCA GCC AAC
    Asp Gly Asp Ala Asp Cys Gln Asp Gly Ser Asp Glu Asp Pro Ala Asn      3876
                        1220                   1225                   1230
    TGT GAG AAG AAG TGC AAC GGC TTC CGC TGC CCG AAC GGC ACC TGC ATT
    Cys Glu Lys Lys Cys Asn Gly Phe Arg Cys Pro Asn Gly Thr Cys Ile      3924
            1235                   1240                   1245
    CCC TCC ACC AAG CAC TGT GAC GGC CTG CAC GAT TGC TCG GAC GGC TCC
    Pro Ser Thr Lys His Cys Asp Gly Leu His Asp Cys Ser Asp Gly Ser      3972
    1250                   1255                   1260                   1265
    GAC GAG CAG CAC TGC GAG CCC CTG TGT ACA CGG TTC ATG GAC TTC GTG
    Asp Glu Gln His Cys Glu Pro Leu Cys Thr Arg Phe Met Asp Phe Val      4020
                1270                   1275                   1280
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TGT AAG AAC CGC CAG CAG TGC CTC TTC CAC TCC ATG CTG TGC GAT GGG    4063
Cys Lys Asn Arg Gln Gln Cys Leu Phe His Ser Met Val Cys Asp Gly
            1285                    1290                1295
ATC ATC CAG TGC CGT GAC GGC TCC GAC GAG GAC CCA GCC TTT GCA GGA    4116
Ile Ile Gln Cys Arg Asp Gly Ser Asp Glu Asp Pro Ala Phe Ala Gly
            1300                    1305                1310
TGC TCC CGA GAC CCC GAG TTC CAC AAG GTG TGC GAT GAG TTC GGC TTC    4164
Cys Ser Arg Asp Pro Glu Phe His Lys Val Cys Asp Glu Phe Gly Phe
            1315                    1320                1325
CAG TGT CAG AAC GGC GTG TGC ATC AGC TTG ATC TGG AAG TGC GAC GGG    4212
Gln Cys Gln Asn Gly Val Cys Ile Ser Leu Ile Trp Lys Cys Asp Gly
    1330                    1335                1340            1345
ATG GAT GAC TGC GGG GAC TAC TCC GAC GAG GCC AAC TGT GAA AAC CCC    4260
Met Asp Asp Cys Gly Asp Tyr Ser Asp Glu Ala Asn Cys Glu Asn Pro
                    1350                    1355                1360
ACA GAA GCC CCC AAC TGC TCC CGC TAC TTC CAG TTC CGG TGT GAC AAT    4308
Thr Glu Ala Pro Asn Cys Ser Arg Tyr Phe Gln Phe Arg Cys Asp Asn
                1365                    1370                1375
GGC CAC TGC ATC CCC AAC AGG TGG AAG TGT GAC AGG GAG AAT GAC TGT    4356
Gly His Cys Ile Pro Asn Arg Trp Lys Cys Asp Arg Glu Asn Asp Cys
                1380                    1385                1390
GGG GAC TGG TCC GAC GAG AAG GAC TGT GGA GAT TCA CAT GTA CTT CCG    4404
Gly Asp Trp Ser Asp Glu Lys Asp Cys Gly Asp Ser His Val Leu Pro
                1395                    1400                1405
TCT ACG ACT CCT GCA CCC TCC ACG TGT CTG CCC AAT TAC TAC CGC TGC    4452
Ser Thr Thr Pro Ala Pro Ser Thr Cys Leu Pro Asn Tyr Tyr Arg Cys
    1410                    1415                1420            1425
GGC GGG GGG GCC TGC GTG ATA GAC ACG TGG GTT TGT GAC GGG TAC CGA    4500
Gly Gly Gly Ala Cys Val Ile Asp Thr Trp Val Cys Asp Gly Tyr Arg
                    1430                    1435                1440
GAT TGC GCA GAT GGA TCC GAC GAG GAA GCC TGC CCC TCG CTC CCC AAT    4548
Asp Cys Ala Asp Gly Ser Asp Glu Glu Ala Cys Pro Ser Leu Pro Asn
                    1445                    1450                1455
GTC ACT GCC ACC TCC TCC CCC TCC CAG CCT GGA CGA TGC GAC CGA TTT    4596
Val Thr Ala Thr Ser Ser Pro Ser Gln Pro Gly Arg Cys Asp Arg Phe
                1460                    1465                1470
GAG TTT GAG TGC CAC CAG CCA AAG AAG TGC ATC CCT AAC TGG AGA CGC    4644
Glu Phe Glu Cys His Gln Pro Lys Lys Cys Ile Pro Asn Trp Arg Arg
            1775                    1480                1485
TGT GAC GGC CAT CAG GAT TGC CAG GAT GGC CAG GAC GAG GCC AAC TGC    4692
Cys Asp Gly His Gln Asp Cys Gln Asp Gly Gln Asp Glu Ala Asn Cys
1490                    1495                1500                1505
CCC ACT CAC AGC ACC TTG ACC TGC ATG AGC TGG GAG TTC AAG TGT GAG    4740
Pro Thr His Ser Thr Leu Thr Cys Met Ser Trp Glu Phe Lys Cys Glu
                    1510                    1515                1520
GAT GGC GAG GCC TGC ATC GTG CTG TCA GAA CGC TGC GAC GGC TTC CTG    4788
Asp Gly Glu Ala Cys Ile Val Leu Ser Glu Arg Cys Asp Gly Phe Leu
                1525                    1530                1535
GAC TGC TCA GAT GAG AGC GAC GAG AAG GCC TGC AGT GAT GAG TTA ACT    4836
Asp Cys Ser Asp Glu Ser Asp Glu Lys Ala Cys Ser Asp Glu Leu Thr
            1540                    1545                1550
GTA TAC AAA GTA CAG AAT CTT CAG TGG ACA GCT GAC TTC TCT GGG AAT    4884
Val Tyr Lys Val Gln Asn Leu Gln Trp Thr Ala Asp Phe Ser Gly Asn
            1555                    1560                1565
GTC ACT TTG ACC TGG ATG CGG CCC AAA AAA ATG CCC TCT GCT GCT TGT    4932
Val Thr Leu Thr Trp Met Arg Pro Lys Lys Met Pro Ser Ala Ala Cys
1570                    1575                1580                1585
GTA TAC AAC GTG TAC TAT AGA GTT GTT GGA GAG AGC ATA TGG AAG ACT    4980
Val Tyr Asn Val Tyr Tyr Arg Val Val Gly Glu Ser Ile Trp Lys Thr
                    1590                    1595                1600
CTG GAG ACT CAC AGC AAT AAG ACA AAC ACT GTA TTA AAA GTG TTG AAA    5028
Leu Glu Thr His Ser Asn Lys Thr Asn Thr Val Leu Lys Val Leu Lys
                    1605                    1610                1615
CCA GAT ACC ACC TAC CAG GTT AAA GTG CAG GTT CAG TGC CTG AGC AAG    5076
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83

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                Pro Asp Thr Thr Tyr Gln Val Lys Val Gln Val Gln Cys Leu Ser Lys
                    1620                1625                1630
5               GTG CAC AAC ACC AAT GAC TTT GTG ACC TTG AGA ACT CCA GAG GGA TTG      5124
                Val His Asn Thr Asn Asp Phe Val Thr Leu Arg Thr Pro Glu Gly Leu
                    1635                1640                1645
                CCA GAC GCC CCT CAG AAC CTC CAG CTG TCG CTC CAC GGG GAA GAG GAA      5172
                Pro Asp Ala Pro Gln Asn Leu Gln Leu Ser Leu His Gly Glu Glu Glu
                1650                1655                1660                1665
10              GGT GTG ATT GTG GGC CAC TGG AGC CCT CCC ACC CAC ACC CAC GGC CTC      5220
                Gly Val Ile Val Gly His Trp Ser Pro Pro Thr His Thr His Gly Leu
                                1670                1675                1680
                ATT CGC GAA TAC ATT GTA GAG TAT AGC AGG AGT GGT TCC AAG GTG TGG      5268
                Ile Arg Glu Tyr Ile Val Glu Tyr Ser Arg Ser Gly Ser Lys Val Trp
                            1685                1690                1695
15              ACT TCA GAA AGG GCT GCT AGT AAC TTT ACA GAA ATA AAG AAC TTG TTG      5316
                Thr Ser Glu Arg Ala Ala Ser Asn Phe Thr Glu Ile Lys Asn Leu Leu
                        1700                1705                1710
                GTC AAC ACC CTG TAC ACC GTC AGA GTG GCT GCG GTG ACG AGT CGT GGG      5364
                Val Asn Thr Leu Tyr Thr Val Arg Val Ala Ala Val Thr Ser Arg Gly
                    1715                1720                1725
                ATA GGA AAC TGG AGC GAT TCC AAA TCC ATT ACC ACC GTG AAA GGA AAA      5412
                Ile Gly Asn Trp Ser Asp Ser Lys Ser Ile Thr Thr Val Lys Gly Lys
20              1730                1735                1740                1745
                GCG ATC CCG CCA CCA AAT ATC CAC ATT GAC AAC TAC GAT GAA AAT TCC      5460
                Ala Ile Pro Pro Pro Asn Ile His Ile Asp Asn Tyr Asp Glu Asn Ser
                                1750                1755                1760
                CTG AGT TTT ACC CTG ACC GTG GAT GGG AAC ATC AAG GTG AAT GGC TAT      5508
                Leu Ser Phe Thr Leu Thr Val Asp Gly Asn Ile Lys Val Asn Gly Tyr
25                          1765                1770                1775
                GTG GTG AAC CTT TTC TGG GCA TTT GAC ACC CAC AAA CAA GAG AAG AAA      5556
                Val Val Asn Leu Phe Trp Ala Phe Asp Thr His Lys Gln Glu Lys Lys
                        1780                1785                1790
                ACC ATG AAC TTC CAA GGG AGC TCA GTG TCC CAC AAA GTT GGC AAT CTG      5604
                Thr Met Asn Phe Gln Gly Ser Ser Val Ser His Lys Val Gly Asn Leu
30                  1795                1800                1805
                ACA GCA CAG ACG GCC TAT GAG ATT TCC GCC TGG GCC AAG ACT GAC TTG      5652
                Thr Ala Gln Thr Ala Tyr Glu Ile Ser Ala Trp Ala Lys Thr Asp Leu
                1810                1815                1820                1825
                GGC GAT AGT CCT CTG TCA TTT GAG CAT GTC ACG ACC AGA GGG GTT CGC      5700
                Gly Asp Ser Pro Leu Ser Phe Glu His Val Thr Thr Arg Gly Val Arg
35                          1830                1835                1840
                CCA CCT GCT CCT AGC CTC AAG GCC AGG GCT ATC AAT CAG ACT GCA GTG      5748
                Pro Pro Ala Pro Ser Leu Lys Ala Arg Ala Ile Asn Gln Thr Ala Val
                            1845                1850                1855
                GAA TGC ACC TGG ACA GGC CCC AGG AAT GTG GTG TAT GGC ATT TTC TAT      5796
                Glu Cys Thr Trp Thr Gly Pro Arg Asn Val Val Tyr Gly Ile Phe Tyr
                    1860                1865                1870
40              GCC ACA TCC TTC CTG GAC CTC TAC CGC AAC CCA AGC AGC CTG ACC ACG      5844
                Ala Thr Ser Phe Leu Asp Leu Tyr Arg Asn Pro Ser Ser Leu Thr Thr
                    1875                1880                1885
                CCG CTG CAC AAC GCA ACC GTG CTC GTC GGT AAG GAT GAG CAG TAT CTG      5892
                Pro Leu His Asn Ala Thr Val Leu Val Gly Lys Asp Glu Gln Tyr Leu
                1890                1895                1900                1905
45              TTT CTG GTC CGG GTG GTG ATG CCC TAC CAA GGG CCG TCC TCG GAC TAC      5940
                Phe Leu Val Arg Val Val Met Pro Tyr Gln Gly Pro Ser Ser Asp Tyr
                                1910                1915                1920
                GTG GTC GTG AAG ATG ATC CCG GAC AGC AGG CTT CCT CCC CGG CAC CTG      5988
                Val Val Val Lys Met Ile Pro Asp Ser Arg Leu Pro Pro Arg His Leu
                            1925                1930                1935
50              CAT GCC GTT CAC ACC GGC AAG ACC TCG GCC GTC ATC AAG TGG GAG TCG      6036
                His Ala Val His Thr Gly Lys Thr Ser Ala Val Ile Lys Trp Glu Ser
                    1940                1945                1950
                CCC TAC GAC TCT CCT GAC CAG GAC CTG TTC TAT GCG ATC GCA GTT AAA      6084
                Pro Tyr Asp Ser Pro Asp Gln Asp Leu Phe Tyr Ala Ile Ala Val Lys
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            1955                    1960                    1965
      GAT CTG ATA CGA AAG ACG GAC CGG AGC TAC AAA GTC AAG TCC CGC AAC   6132
      Asp Leu Ile Arg Lys Thr Asp Arg Ser Tyr Lys Val Lys Ser Arg Asn
            1970                    1975                    1980            1985
      AGC ACC GTG GAG TAC ACC CTG AGC AAG CTG GAG CCC GGA GGG AAA TAC   6180
      Ser Thr Val Glu Tyr Thr Leu Ser Lys Leu Glu Pro Gly Gly Lys Tyr
                                1990                    1995            2000
      CAC GTC ATT GTG CAG CTG GGG AAC ATG AGC AAA GAT GCC AGT GTG AAG   6228
      His Val Ile Val Gln Leu Gly Asn Met Ser Lys Asp Ala Ser Val Lys
                            2005                    2010            2015
      ATC ACC ACC GTT TCG TTA TCG GCA CCC GAT GCC TTA AAA ATC ATA ACA   6276
      Ile Thr Thr Val Ser Leu Ser Ala Pro Asp Ala Leu Lys Ile Ile Thr
                            2020                    2025            2030
      GAA AAT GAC CAC GTC CTT CTC TTC TGG AAA AGT CTA GCT CTA AAG GAA   6324
      Glu Asn Asp His Val Leu Leu Phe Trp Lys Ser Leu Ala Leu Lys Glu
                            2035                    2040            2045
      AAG TAT TTT AAC GAA AGC AGG GGC TAC GAG ATA CAC ATG TTT GAT AGC   6372
      Lys Tyr Phe Asn Glu Ser Arg Gly Tyr Glu Ile His Met Phe Asp Ser
            2050                    2055                    2060            2065
      GCC ATG AAT ATC ACC GCA TAC CTT GGG AAT ACT ACT GAC AAT TTC TTT   6420
      Ala Met Asn Ile Thr Ala Tyr Leu Gly Asn Thr Thr Asp Asn Phe Phe
                                2070                    2075            2080
      AAA ATT TCC AAC CTG AAG ATG GGT CAC AAT TAC ACA TTC ACG GTC CAG   6468
      Lys Ile Ser Asn Leu Lys Met Gly His Asn Tyr Thr Phe Thr Val Gln
                            2085                    2090            2095
      GCA CGA TGC CTT TTG GGC AGC CAG ATC TGC GGG GAG CCT GCC GTG CTA   6516
      Ala Arg Cys Leu Leu Gly Ser Gln Ile Cys Gly Glu Pro Ala Val Leu
                            2100                    2105            2110
      CTG TAT GAT GAG CTG GGG TCT GGT GGC GAT GCG TCG GCG ATG CAG GCT   6564
      Leu Tyr Asp Glu Leu Gly Ser Gly Gly Asp Ala Ser Ala Met Gln Ala
            2115                    2120                    2125
      GCC AGG TCT ACT GAT GTC GCC GCC GTG GTG GTG CCC ATC CTG TTT CTG   6612
      Ala Arg Ser Thr Asp Val Ala Ala Val Val Val Pro Ile Leu Phe Leu
            2130                    2135                    2140            2145
      ATA CTG CTG AGC CTG GGG GTC GGG TTT GCC ATC CTG TAC ACG AAG CAT   6660
      Ile Leu Leu Ser Leu Gly Val Gly Phe Ala Ile Leu Tyr Thr Lys His
                            2150                    2155            2160
      CGG AGG CTG CAG AGC AGC TTC ACC GCC TTC GCC AAC AGC CAC TAC AGC   6708
      Arg Arg Leu Gln Ser Ser Phe Thr Ala Phe Ala Asn Ser His Tyr Ser
                            2165                    2170            2175
      TCC AGA CTC GGC TCC GCC ATC TTC TCC TCT GGG GAT GAC TTG GGG GAG   6756
      Ser Arg Leu Gly Ser Ala Ile Phe Ser Ser Gly Asp Asp Leu Gly Glu
                            2180                    2185            2190
      GAT GAT GAA GAT GCT CCT ATG ATC ACT GGA TTT TCG GAC GAC GTC CCC   6804
      Asp Asp Glu Asp Ala Pro Met Ile Thr Gly Phe Ser Asp Asp Val Pro
            2195                    2200                    2205
      ATG GTG ATA GCC TGAAAGAGCT TTCCTCACTA GAAACCAAAT GGTGTAAATA       6856
      Met Val Ile Ala
            2210
      TTTTATTTGA TAAAGATAGT TGATGGTTTA TTTTAAAAGA TGCACTTTGA GTTGCAATAT 6916
      GTTATTTTTA TATGGGCCAA AAACAAAAGC AAAAAAAAAA AAAAA                 6961
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(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 300 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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ATATCCACAT TGACAGCTAT GGTGAAAATT ATCTAAGCTT CACCCTGACC ATGGAGAGTG      60

ATATCAAGGT GAATGGCTAT GTGGTGAACC TTTTCTGGGC ATTTGACACC CACAAGCAAG     120

AGAGGAGAAC TTTGAACTTC CGAGGAAGCA TATTGTCACA CAAAGTTGGC AATCTGACAG     180

CTCATACATC CTATGAGATT TCTGCCTGGG CCAAGACTGA CTTGGGGGAT AGCCCTCTGG     240

CATTTGAGCA TGTTATGACC AGAGGGGTTC GCCCACCTGC ACCTAGCCTC AAGGCCAAAG     300
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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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ATGGCGACAC GGAGCAGCAG GAGGGAGTCG CGACTCCCGT TCCTATTCAC CCTGGTCGCA      60

CTGCTGCCGC CCGGAGCTCT CTGCGAAGTC TGGACGCAGA GGCTGCACGG CGGCAGCGCG     120

CCCTTGCCCC AGGACCGGGG CTTCCTCGTG GTGCAGGGCG ACCCGCGCGA GCTGCGGCTG     180

TGGGCGCGCG GGGATGCCAG GGGGGCGAGC CGCGCGGACG AGAAGCCGCT CCGGAGGAAA     240

CGGAGCGCTG CCCTGCAGCC CGAGCCCATC AAGGTGTACG GACAGGTTAG TCTGAATGAT     300

TCCCACAATC AGATGGTGGT GCACTGGGCT GGAGAGAAAA GCAACGTGAT CGTGGCCTTG     360

GCCCGAGATA GCCTGGCATT GGCGAGGCCC AAGAGCAGTG ATGTGTACGT GTCTTACGAC     420

TATGGAAAAT CATTCAAGAA AATTTCAGAC AAGTTAAACT TTGGCTTGGG AAATAGGAGT     480

GAAGCTGTTA TCGCCCAGTT CTACCACAGC CCTGCGGACA CAAGCGGTA CATCTTTGCA      540

GACGCTTATG CCCAGTACCT CTGGATCACG TTTGACTTCT GCAACACTCT TCAAGGCTTT     600

TCCATCCCAT TTCGGGCAGC TGATCTCCTC CTACACAGTA AGGCCTCCAA CCTTCTCTTG     660

GGCTTTGACA GGTCCCACCC CAACAAGCAG CTGTGGAAGT CAGATGACTT TGGCCAGACC     720

TGGATCATGA TTCAGGAACA TGTCAAGTCC TTTTCTTGGG GAATTGATCC CTATGACAAA     780

CCAAATACCA TCTACATTGA ACGACACGAA CCCTCTGGCT ACTCCACTGT CTTCCGAAGT     840

ACAGATTTCT TCCAGTCCCG GGAAAACCAG GAAGTGATCC TTGAGGAAGT GAGAGATTTT     900

CAGCTTCGGG ACAAGTACAT GTTTGCTACA AAGGTGGTGC ATCTCTTGGG CAGTGAACAG     960

CAGTCTTCTG TCCAGCTCTG GGTCTCCTTT GGCCGGAAGC CCATGAGAGC AGCCCAGTTT    1020

GTCACAAGAC ATCCTATTAA TGAATATTAC ATCGCAGATG CCTCCGAGGA CCAGGTGTTT    1080
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GTGTGTGTCA GCCACAGTAA CAACCGCACC AATTTATACA TCTCAGAGGC AGAGGGGCTG    1140

AAGTTCTCCC TGTCCTTGGA GAACGTGCTC TATTACAGCC CAGGAGGGGC CGGCAGTGAC    1200

ACCTTGGTGA GGTATTTTGC AAATGAACCA TTTGCTGACT TCCACCGAGT GGAAGGATTG    1260

CAAGGAGTCT ACATTGCTAC TCTGATTAAT GGTTCTATGA ATGAGGAGAA CATGAGATCG    1320

GTCATCACCT TTGACAAAGG GGGAACCTGG GAGTTTCTTC AGGCTCCAGC CTTCACGGGA    1380

TATGGAGAGA AAATCAATTG TGAGCTTTCC CAGGGCTGTT CCCTTCATCT GGCTCAGCGC    1440

CTCAGTCAGC TCCTCAACCT CCAGCTCCGG AGAATGCCCA TCCTGTCCAA GGAGTCGGCT    1500

CCAGGCCTCA TCATCGCCAC TGGCTCAGTG GGAAAGAACT TGGCTAGCAA GACAAACGTG    1560

TACATCTCTA GCAGTGCTGG AGCCAGGTGG CGAGAGGCAC TTCCTGGACC TCACTACTAC    1620

ACATGGGGAG ACCACGGCGG AATCATCACG GCCATTGCCC AGGGCATGGA AACCAACGAG    1680

CTAAAATACA GTACCAATGA AGGGGAGACC TGGAAAACAT TCATCTTCTC TGAGAAGCCA    1740

GTGTTTGTGT ATGGCCTCCT CACAGAACCT GGGGAGAAGA GCACTGTCTT CACCATCTTT    1800

GGCTCGAACA AAGAGAATGT CCACAGCTGG CTGATCCTCC AGGTCAATGC CACGGATGCC    1860

TTGGGAGTTC CCTGCACAGA GAATGACTAC AAGCTGTGGT CACCATCTGA TGAGCGGGGG    1920

AATGAGTGTT TGCTGGGACA CAAGACTGTT TTCAAACGGC GGACCCCCCA TGCCACATGC    1980

TTCAATGGAG AGGACTTTGA CAGGCCGGTG GTCGTGTCCA ACTGCTCCTG CACCCGGGAG    2040

GACTATGAGT GTGACTTCGG TTTCAAGATG AGTGAAGATT TGTCATTAGA GGTTTGTGTT    2100

CCAGATCCGG AATTTTCTGG AAAGTCATAC TCCCCTCCTG TGCCTTGCCC TGTGGGTTCT    2160

ACTTACAGGA GAACGAGAGG CTACCGGAAG ATTTCTGGGG ACACTTGTAG CGGAGGAGAT    2220

GTTGAAGCGC GACTGGAAGG AGAGCTGGTC CCCTGTCCCC TGGCAGAAGA GAACGAGTTC    2280

ATTCTGTATG CTGTGAGGAA ATCCATCTAC CGCTATGACC TGGCCTCGGG AGCCACCGAG    2340

CAGTTGCCTC TCACCGGGCT ACGGGCAGCA GTGGCCCTGG ACTTTGACTA TGAGCACAAC    2400

TGTTTGTATT GGTCCGACCT GGCCTTGGAC GTCATCCAGC GCCTCTGTTT GAATGGAAGC    2460

ACAGGGCAAG AGGTGATCAT CAATTCTGGC CTGGAGACAG TAGAAGCTTT GGCTTTTGAA    2520

CCCCTCAGCC AGCTGCTTTA CTGGGTAGAT GCAGGCTTCA AAAAGATTGA GGTAGCTAAT    2580

CCAGATGGCG ACTTCCGACT CACAATCGTC AATTCCTCTG TGCTTGATCG TCCCAGGGCT    2640

CTGGTCCTCG TGCCCCAAGA GGGGGTGATG TTCTGGACAG ACTGGGGAGA CCTGAAGCCT    2700

GGGATTTATC GGAGCAATAT GGATGGTTCT GCTGCCTATC ACCTGGTGTC TGAGGATGTG    2760

AAGTGGCCCA ATGGCATCTC TGTGGACGAC CAGTGGATTT ACTGGACGGA TGCCTACCTG    2820

GAGTGCATAG AGCGGATCAC GTTCAGTGGC CAGCAGCGCT CTGTCATTCT GGACAACCTC    2880

CCGCACCCCT ATGCCATTGC TGTCTTTAAG AATGAAATCT ACTGGGATGA CTGGTCACAG    2940

CTCAGCATAT TCCGAGCTTC CAAATACAGT GGGTCCCAGA TGGAGATTCT GGCAAACCAG    3000
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CTCACGGGGC TCATGGACAT GAAGATTTTC TACAAGGGGA AGAACACTGG AAGCAATGCC   3060

TGTGTGCCCA GGCCATGCAG CCTGCTGTGC CTGCCCAAGG CCAACAACAG TAGAAGCTGC   3120

AGGTGTCCAG AGGATGTGTC CAGCAGTGTG CTTCCATCAG GGGACCTGAT GTGTGACTGC   3180

CCTCAGGGCT ATCAGCTCAA GAACAATACC TGTGTCAAAG AAGAGAACAC CTGTCTTCGC   3240

AACCAGTATC GCTGCAGCAA CGGGAACTGT ATCAACAGCA TTTGGTGGTG TGACTTTGAC   3300

AACGACTGTG AGACATGAG CGATGAGAGA AACTGCCCTA CCACCATCTG TGACCTGGAC    3360

ACCCAGTTTC GTTGCCAGGA GTCTGGGACT TGTATCCCAC TGTCCTATAA ATGTGACCTT   3420

GAGGATGACT GTGGAGACAA CAGTGATGAA AGTCATTGTG AAATGCACCA GTGCCGGAGT   3480

GACGAGTACA ACTGCAGTTC CGGCATGTGC ATCCGCTCCT CCTGGGTATG TGACGGGGAC   3540

AACGACTGCA GGGACTGGTC TGATGAAGCC AACTGTACCG CCATCTATCA CACCTGTGAG   3600

GCCTCCAACT TCCAGTGCCG AAACGGGCAC TGCATCCCCC AGCGGTGGGC GTGTGACGGG   3660

GATACGGACT GCCAGGATGG TTCCGATGAG GATCCAGTCA ACTGTGAGAA GAAGTGCAAT   3720

GGATTCCGCT GCCCAAACGG CACTTGCATC CCATCCAGCA AACATTGTGA TGGTCTGCGT   3780

GATTGCTCTG ATGGCTCCGA TGAACAGCAC TGCGAGCCCC TCTGTACGCA CTTCATGGAC   3840

TTTGTGTGTA AGAACCGCCA GCAGTGCCTG TTCCACTCCA TGGTCTGTGA CGGAATCATC   3900

CAGTGCCGCG ACGGGTCCGA TGAGGATGCG GCGTTTGCAG GATGCTCCCA AGATCCTGAG   3960

TTCCACAAGG TATGTGATGA GTTCGGTTTC CAGTGTCAGA ATGGAGTGTG CATCAGTTTG   4020

ATTTGGAAGT GCGACGGGAT GGATGATTGC GGCGATTATT CTGATGAAGC CAACTGCGAA   4080

AACCCCACAG AAGCCCCAAA CTGCTCCCGC TACTTCCAGT TTCGGTGTGA GAATGGCCAC   4140

TGCATCCCCA ACAGATGGAA ATGTGACAGG GAGAACGACT GTGGGGACTG GTCTGATGAG   4200

AAGGATTGTG GAGATTCACA TATTCTTCCC TTCTCGACTC CTGGGCCCTC CACGTGTCTG   4260

CCCAATTACT ACCGCTGCAG CAGTGGGACC TGCGTGATGG ACACCTGGGT GTGCGACGGG   4320

TACCGAGATT GTGCAGATGG CTCTGACGAG GAAGCCTGCC CCTTGCTTGC AAACGTCACT   4380

GCTGCCTCCA CTCCCACCCA ACTTGGGCGA TGTGACCGAT TTGAGTTCGA ATGCCACCAA   4440

CCGAAGACGT GTATTCCCAA CTGGAAGCGC TGTGACGGCC ACCAAGATTG CCAGGATGGC   4500

CGGGACGAGG CCAATTGCCC CACACACAGC ACCTTGACTT GCATGAGCAG GGAGTTCCAG   4560

TGCGAGGACG GGGAGGCCTG CATTGTGCTC TCGGAGCGCT GCGACGGCTT CCTGGACTGC   4620

TCGGACGAGA GCGATGAAAA GGCCTGCAGT GATGAGTTGA CTGTGTACAA AGTACAGAAT   4680

CTTCAGTGGA CAGCTGACTT CTCTGGGGAT GTGACTTTGA CCTGGATGAG GCCCAAAAAA   4740

ATGCCCTCTG CATCTTGTGT ATATAATGTC TACTACAGGG TGGTTGGAGA GAGCATATGG   4800

AAGACTCTGG AGACCCACAG CAATAAGACA AACACTGTAT TAAAAGTCTT GAAACCAGAT   4860

ACCACGTATC AGGTTAAAGT ACAGGTTCAG TGTCTCAGCA AGGCACACAA CACCAATGAC   4920
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TTTGTGACCC TGAGGACCCC AGAGGGATTG CCAGATGCCC CTCGAAATCT CCAGCTGTCA    4980

CTCCCCAGGG AAGCAGAAGG TGTGATTGTA GGCCACTGGG CTCCTCCCAT CCACACCCAT    5040

GGCCTCATCC GTGAGTACAT TGTAGAATAC AGCAGGAGTG GTTCCAAGAT GTGGGCCTCC    5100

CAGAGGGCTG CTAGTAACTT TACAGAAATC AAGAACTTAT TGGTCAACAC TCTATACACC    5160

GTCAGAGTGG CTGCGGTGAC TAGTCGTGGA ATAGGAAACT GGAGCGATTC TAAATCCATT    5220

ACCACCATAA AAGGAAAAGT GATCCCACCA CCAGATATCC ACATTGACAG CTATGGTGAA    5280

AATTATCTAA GCTTCACCCT GACCATGGAG AGTGATATCA AGGTGAATGG CTATGTGGTG    5340

AACCTTTTCT GGGCATTTGA CACCCACAAG CAAGAGAGGA GAACTTTGAA CTTCCGAGGA    5400

AGCATATTGT CACACAAAGT TGGCAATCTG ACAGCTCATA CATCCTATGA GATTTCTGCC    5460

TGGGCCAAGA CTGACTTGGG GGATAGCCCT CTGGCATTTG AGCATGTTAT GACCAGAGGG    5520

GTTCGCCCAC CTGCACCTAG CCTCAAGGCC AAAGCCATCA ACCAGACTGC AGTGGAATGT    5580

ACCTGGACCG GCCCCCGGAA TGTGGTTTAT GGTATTTTCT ATGCCACGTC CTTTCTTGAC    5640

CTCTATCGCA ACCCGAAGAG CTTGACTACT TCACTCCACA ACAAGACGGT CATTGTCAGT    5700

AAGGATGAGC AGTATTTGTT TCTGGTCCGT GTAGTGGTAC CCTACCAGGG GCCATCCTCT    5760

GACTACGTTG TAGTGAAGAT GATCCCGGAC AGCAGGCTTC CACCCCGTCA CCTGCATGTG    5820

GTTCATACGG GCAAAACCTC CGTGGTCATC AAGTGGGAAT CACCGTATGA CTCTCCTGAC    5880

CAGGACTTGT TGTATGCAAT TGCAGTCAAA GATCTCATAA GAAAGACTGA CAGGAGCTAC    5940

AAAGTAAAAT CCCGTAACAG CACTGTGGAA TACACCCTTA ACAAGTTGGA GCCTGGCGGG    6000

AAATACCACA TCATTGTCCA ACTGGGGAAC ATGAGCAAAG ATTCCAGCAT AAAAATTACC    6060

ACAGTTTCAT TATCAGCACC TGATGCCTTA AAAATCATAA CAGAAAATGA TCATGTTCTT    6120

CTGTTTTGGA AAAGCCTGGC TTTAAAGGAA AAGCATTTTA ATGAAAGCAG GGGCTATGAG    6180

ATACACATGT TTGATAGTGC CATGAATATC ACAGCTTACC TTGGGAATAC TACTGACAAT    6240

TTCTTTAAAA TTTCCAACCT GAAGATGGGT CATAATTACA CGTTCACCGT CCAAGCAAGA    6300

TGCCTTTTTG GCAACCAGAT CTGTGGGGAG CCTGCCATCC TGCTGTACGA TGAGCTGGGG    6360

TCTGGTGCAG ATGCATCTGC AACGCAGGCT GCCAGATCTA CGGATGTTGC TGCTGTGGTG    6420

GTGCCCATCT TATTCCTGAT ACTGCTGAGC CTGGGGGTGG GGTTTGCCAT CCTGTACACG    6480

AAGCACCGGA GGCTGCAGAG CAGCTTCACC GCCTTCGCCA ACAGCCACTA CAGCTCCAGG    6540

CTGGGGTCCG CAATCTTCTC CTCTGGGGAT GACCTGGGGG AAGATGATGA AGATGCCCCT    6600

ATGATAACTG GATTTTCAGA TGACGTCCCC ATGGTGATAG CC                        6642
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(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2214 amino acids
        (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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Met Ala Thr Arg Ser Ser Arg Arg Glu Ser Arg Leu Pro Phe Leu Phe
1               5                   10              15

Thr Leu Val Ala Leu Leu Pro Pro Gly Ala Leu Cys Glu Val Trp Thr
            20              25                  30

Gln Arg Leu His Gly Gly Ser Ala Pro Leu Pro Gln Asp Arg Gly Phe
            35              40                  45

Leu Val Val Gln Gly Asp Pro Arg Glu Leu Arg Leu Trp Ala Arg Gly
            50              55                  60

Asp Ala Arg Gly Ala Ser Arg Ala Asp Glu Lys Pro Leu Arg Arg Lys
65              70                  75                  80

Arg Ser Ala Ala Leu Gln Pro Glu Pro Ile Lys Val Tyr Gly Gln Val
                85                  90                  95

Ser Leu Asn Asp Ser His Asn Gln Met Val Val His Trp Ala Gly Glu
                100             105                 110

Lys Ser Asn Val Ile Val Ala Leu Ala Arg Asp Ser Leu Ala Leu Ala
                115             120                 125

Arg Pro Lys Ser Ser Asp Val Tyr Val Ser Tyr Asp Tyr Gly Lys Ser
        130             135             140

Phe Lys Lys Ile Ser Asp Lys Leu Asn Phe Gly Leu Gly Asn Arg Ser
145             150             155                 160

Glu Ala Val Ile Ala Gln Phe Tyr His Ser Pro Ala Asp Asn Lys Arg
                165             170                 175

Tyr Ile Phe Ala Asp Ala Tyr Ala Gln Tyr Leu Trp Ile Thr Phe Asp
            180             185             190

Phe Cys Asn Thr Leu Gln Gly Phe Ser Ile Pro Phe Arg Ala Ala Asp
            195             200             205

Leu Leu Leu His Ser Lys Ala Ser Asn Leu Leu Leu Gly Phe Asp Arg
    210             215             220

Ser His Pro Asn Lys Gln Leu Trp Lys Ser Asp Asp Phe Gly Gln Thr
225             230             235                 240

Trp Ile Met Ile Gln Glu His Val Lys Ser Phe Ser Trp Gly Ile Asp
                245             250                 255

Pro Tyr Asp Lys Pro Asn Thr Ile Tyr Ile Glu Arg His Glu Pro Ser
            260             265                 270

Gly Tyr Ser Thr Val Phe Arg Ser Thr Asp Phe Phe Gln Ser Arg Glu
            275             280                 285
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Asn Gln Glu Val Ile Leu Glu Glu Val Arg Asp Phe Gln Leu Arg Asp
    290              295              300
Lys Tyr Met Phe Ala Thr Lys Val Val His Leu Leu Gly Ser Glu Gln
305              310              315              320
Gln Ser Ser Val Gln Leu Trp Val Ser Phe Gly Arg Lys Pro Met Arg
                325              330              335
Ala Ala Gln Phe Val Thr Arg His Pro Ile Asn Glu Tyr Tyr Ile Ala
            340              345              350
Asp Ala Ser Glu Asp Gln Val Phe Val Cys Val Ser His Ser Asn Asn
            355              360              365
Arg Thr Asn Leu Tyr Ile Ser Glu Ala Glu Gly Leu Lys Phe Ser Leu
    370              375              380
Ser Leu Glu Asn Val Leu Tyr Tyr Ser Pro Gly Gly Ala Gly Ser Asp
385              390              395              400
Thr Leu Val Arg Tyr Phe Ala Asn Glu Pro Phe Ala Asp Phe His Arg
            405              410              415
Val Glu Gly Leu Gln Gly Val Tyr Ile Ala Thr Leu Ile Asn Gly Ser
            420              425              430
Met Asn Glu Glu Asn Met Arg Ser Val Ile Thr Phe Asp Lys Gly Gly
    435              440              445
Thr Trp Glu Phe Leu Gln Ala Pro Ala Phe Thr Gly Tyr Gly Glu Lys
    450              455              460
Ile Asn Cys Glu Leu Ser Gln Gly Cys Ser Leu His Leu Ala Gln Arg
465              470              475              480
Leu Ser Gln Leu Leu Asn Leu Gln Leu Arg Arg Met Pro Ile Leu Ser
            485              490              495
Lys Glu Ser Ala Pro Gly Leu Ile Ile Ala Thr Gly Ser Val Gly Lys
            500              505              510
Asn Leu Ala Ser Lys Thr Asn Val Tyr Ile Ser Ser Ser Ala Gly Ala
    515              520              525
Arg Trp Arg Glu Ala Leu Pro Gly Pro His Tyr Tyr Thr Trp Gly Asp
    530              535              540
His Gly Gly Ile Ile Thr Ala Ile Ala Gln Gly Met Glu Thr Asn Glu
545              550              555              560
Leu Lys Tyr Ser Thr Asn Glu Gly Glu Thr Trp Lys Thr Phe Ile Phe
            565              570              575
Ser Glu Lys Pro Val Phe Val Tyr Gly Leu Leu Thr Glu Pro Gly Glu
            580              585              590
Lys Ser Thr Val Phe Thr Ile Phe Gly Ser Asn Lys Glu Asn Val His
            595              600              605
Ser Trp Leu Ile Leu Gln Val Asn Ala Thr Asp Ala Leu Gly Val Pro
    610              615              620
Cys Thr Glu Asn Asp Tyr Lys Leu Trp Ser Pro Ser Asp Glu Arg Gly
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          625                    630                    635                    640

          Asn Glu Cys Leu Leu Gly His Lys Thr Val Phe Lys Arg Arg Thr Pro
5                         645                 650                 655

          His Ala Thr Cys Phe Asn Gly Glu Asp Phe Asp Arg Pro Val Val Val
                          660                 665                 670

          Ser Asn Cys Ser Cys Thr Arg Glu Asp Tyr Glu Cys Asp Phe Gly Phe
10                        675                 680                 685

          Lys Met Ser Glu Asp Leu Ser Leu Glu Val Cys Val Pro Asp Pro Glu
                          690                 695                 700

          Phe Ser Gly Lys Ser Tyr Ser Pro Pro Val Pro Cys Pro Val Gly Ser
15        705                 710                 715                 720

          Thr Tyr Arg Arg Thr Arg Gly Tyr Arg Lys Ile Ser Gly Asp Thr Cys
                              725                 730                 735

          Ser Gly Gly Asp Val Glu Ala Arg Leu Glu Gly Glu Leu Val Pro Cys
20                        740                 745                 750

          Pro Leu Ala Glu Glu Asn Glu Phe Ile Leu Tyr Ala Val Arg Lys Ser
                          755                 760                 765

          Ile Tyr Arg Tyr Asp Leu Ala Ser Gly Ala Thr Glu Gln Leu Pro Leu
                          770                 775                 780

25        Thr Gly Leu Arg Ala Ala Val Ala Leu Asp Phe Asp Tyr Glu His Asn
          785                 790                 795                 800

          Cys Leu Tyr Trp Ser Asp Leu Ala Leu Asp Val Ile Gln Arg Leu Cys
                              805                 810                 815

30        Leu Asn Gly Ser Thr Gly Gln Glu Val Ile Ile Asn Ser Gly Leu Glu
                              820                 825                 830

          Thr Val Glu Ala Leu Ala Phe Glu Pro Leu Ser Gln Leu Leu Tyr Trp
                          835                 840                 845

35        Val Asp Ala Gly Phe Lys Lys Ile Glu Val Ala Asn Pro Asp Gly Asp
              850                 855                 860

          Phe Arg Leu Thr Ile Val Asn Ser Ser Val Leu Asp Arg Pro Arg Ala
          865                 870                 875                 880

40        Leu Val Leu Val Pro Gln Glu Gly Val Met Phe Trp Thr Asp Trp Gly
                          885                 890                 895

          Asp Leu Lys Pro Gly Ile Tyr Arg Ser Asn Met Asp Gly Ser Ala Ala
                          900                 905                 910

45        Tyr His Leu Val Ser Glu Asp Val Lys Trp Pro Asn Gly Ile Ser Val
              915                 920                 925

          Asp Asp Gln Trp Ile Tyr Trp Thr Asp Ala Tyr Leu Glu Cys Ile Glu
              930                 935                 940

50        Arg Ile Thr Phe Ser Gly Gln Gln Arg Ser Val Ile Leu Asp Asn Leu
          945                 950                 955                 960

          Pro His Pro Tyr Ala Ile Ala Val Phe Lys Asn Glu Ile Tyr Trp Asp
                          965                 970                 975
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Asp Trp Ser Gln Leu Ser Ile Phe Arg Ala Ser Lys Tyr Ser Gly Ser
          980                     985               990

Gln Met Glu Ile Leu Ala Asn Gln Leu Thr Gly Leu Met Asp Met Lys
          995                 1000              1005

Ile Phe Tyr Lys Gly Lys Asn Thr Gly Ser Asn Ala Cys Val Pro Arg
         1010              1015              1020

Pro Cys Ser Leu Leu Cys Leu Pro Lys Ala Asn Asn Ser Arg Ser Cys
1025              1030              1035              1040

Arg Cys Pro Glu Asp Val Ser Ser Ser Val Leu Pro Ser Gly Asp Leu
             1045              1050              1055

Met Cys Asp Cys Pro Gln Gly Tyr Gln Leu Lys Asn Asn Thr Cys Val
         1060              1065              1070

Lys Glu Glu Asn Thr Cys Leu Arg Asn Gln Tyr Arg Cys Ser Asn Gly
         1075              1080              1085

Asn Cys Ile Asn Ser Ile Trp Trp Cys Asp Phe Asp Asn Asp Cys Gly
         1090              1095              1100

Asp Met Ser Asp Glu Arg Asn Cys Pro Thr Thr Ile Cys Asp Leu Asp
1105              1110              1115              1120

Thr Gln Phe Arg Cys Gln Glu Ser Gly Thr Cys Ile Pro Leu Ser Tyr
             1125              1130              1135

Lys Cys Asp Leu Glu Asp Asp Cys Gly Asp Asn Ser Asp Glu Ser His
         1140              1145              1150

Cys Glu Met His Gln Cys Arg Ser Asp Glu Tyr Asn Cys Ser Ser Gly
         1155              1160              1165

Met Cys Ile Arg Ser Ser Trp Val Cys Asp Gly Asp Asn Asp Cys Arg
    1170              1175              1180

Asp Trp Ser Asp Glu Ala Asn Cys Thr Ala Ile Tyr His Thr Cys Glu
1185              1190              1195              1200

Ala Ser Asn Phe Gln Cys Arg Asn Gly His Cys Ile Pro Gln Arg Trp
             1205              1210              1215

Ala Cys Asp Gly Asp Thr Asp Cys Gln Asp Gly Ser Asp Glu Asp Pro
         1220              1225              1230

Val Asn Cys Glu Lys Lys Cys Asn Gly Phe Arg Cys Pro Asn Gly Thr
         1235              1240              1245

Cys Ile Pro Ser Ser Lys His Cys Asp Gly Leu Arg Asp Cys Ser Asp
    1250              1255              1260

Gly Ser Asp Glu Gln His Cys Glu Pro Leu Cys Thr His Phe Met Asp
1265              1270              1275              1280

Phe Val Cys Lys Asn Arg Gln Gln Cys Leu Phe His Ser Met Val Cys
             1285              1290              1295

Asp Gly Ile Ile Gln Cys Arg Asp Gly Ser Asp Glu Asp Ala Ala Phe
         1300              1305              1310
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Ala Gly Cys Ser Gln Asp Pro Glu Phe His Lys Val Cys Asp Glu Phe
  1315   1320   1325

Gly Phe Gln Cys Gln Asn Gly Val Cys Ile Ser Leu Ile Trp Lys Cys
  1330   1335   1340

Asp Gly Met Asp Asp Cys Gly Asp Tyr Ser Asp Glu Ala Asn Cys Glu
1345   1350   1355   1360

Asn Pro Thr Glu Ala Pro Asn Cys Ser Arg Tyr Phe Gln Phe Arg Cys
    1365   1370   1375

Glu Asn Gly His Cys Ile Pro Asn Arg Trp Lys Cys Asp Arg Glu Asn
    1380   1385   1390

Asp Cys Gly Asp Trp Ser Asp Glu Lys Asp Cys Gly Asp Ser His Ile
    1395   1400   1405

Leu Pro Phe Ser Thr Pro Gly Pro Ser Thr Cys Leu Pro Asn Tyr Tyr
  1410   1415   1420

Arg Cys Ser Ser Gly Thr Cys Val Met Asp Thr Trp Val Cys Asp Gly
1425   1430   1435   1440

Tyr Arg Asp Cys Ala Asp Gly Ser Asp Glu Glu Ala Cys Pro Leu Leu
    1445   1450   1455

Ala Asn Val Thr Ala Ala Ser Thr Pro Thr Gln Leu Gly Arg Cys Asp
    1460   1465   1470

Arg Phe Glu Phe Glu Cys His Gln Pro Lys Thr Cys Ile Pro Asn Trp
  1475   1480   1485

Lys Arg Cys Asp Gly His Gln Asp Cys Gln Asp Gly Arg Asp Glu Ala
  1490   1495   1500

Asn Cys Pro Thr His Ser Thr Leu Thr Cys Met Ser Arg Glu Phe Gln
1505   1510   1515   1520

Cys Glu Asp Gly Glu Ala Cys Ile Val Leu Ser Glu Arg Cys Asp Gly
    1525   1530   1535

Phe Leu Asp Cys Ser Asp Glu Ser Asp Glu Lys Ala Cys Ser Asp Glu
    1540   1545   1550

Leu Thr Val Tyr Lys Val Gln Asn Leu Gln Trp Thr Ala Asp Phe Ser
    1555   1560   1565

Gly Asp Val Thr Leu Thr Trp Met Arg Pro Lys Lys Met Pro Ser Ala
  1570   1575   1580

Ser Cys Val Tyr Asn Val Tyr Tyr Arg Val Val Gly Glu Ser Ile Trp
1585   1590   1595   1600

Lys Thr Leu Glu Thr His Ser Asn Lys Thr Asn Thr Val Leu Lys Val
    1605   1610   1615

Leu Lys Pro Asp Thr Thr Tyr Gln Val Lys Val Gln Val Gln Cys Leu
    1620   1625   1630

Ser Lys Ala His Asn Thr Asn Asp Phe Val Thr Leu Arg Thr Pro Glu
    1635   1640   1645

Gly Leu Pro Asp Ala Pro Arg Asn Leu Gln Leu Ser Leu Pro Arg Glu

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            1650                    1655                    1660

     Ala Glu Gly Val Ile Val Gly His Trp Ala Pro Pro Ile His Thr His
     1665               1670               1675               1680

     Gly Leu Ile Arg Glu Tyr Ile Val Glu Tyr Ser Arg Ser Gly Ser Lys
                    1685               1690               1695

     Met Trp Ala Ser Gln Arg Ala Ala Ser Asn Phe Thr Glu Ile Lys Asn
                    1700               1705               1710

     Leu Leu Val Asn Thr Leu Tyr Thr Val Arg Val Ala Ala Val Thr Ser
                    1715               1720               1725

     Arg Gly Ile Gly Asn Trp Ser Asp Ser Lys Ser Ile Thr Thr Ile Lys
                    1730               1735               1740

     Gly Lys Val Ile Pro Pro Pro Asp Ile His Ile Asp Ser Tyr Gly Glu
     1745               1750               1755               1760

     Asn Tyr Leu Ser Phe Thr Leu Thr Met Glu Ser Asp Ile Lys Val Asn
                    1765               1770               1775

     Gly Tyr Val Val Asn Leu Phe Trp Ala Phe Asp Thr His Lys Gln Glu
                    1780               1785               1790

     Arg Arg Thr Leu Asn Phe Arg Gly Ser Ile Leu Ser His Lys Val Gly
                    1795               1800               1805

     Asn Leu Thr Ala His Thr Ser Tyr Glu Ile Ser Ala Trp Ala Lys Thr
                    1810               1815               1820

     Asp Leu Gly Asp Ser Pro Leu Ala Phe Glu His Val Met Thr Arg Gly
     1825               1830               1835               1840

     Val Arg Pro Pro Ala Pro Ser Leu Lys Ala Lys Ala Ile Asn Gln Thr
                    1845               1850               1855

     Ala Val Glu Cys Thr Trp Thr Gly Pro Arg Asn Val Val Tyr Gly Ile
                    1860               1865               1870

     Phe Tyr Ala Thr Ser Phe Leu Asp Leu Tyr Arg Asn Pro Lys Ser Leu
                    1875               1880               1885

     Thr Thr Ser Leu His Asn Lys Thr Val Ile Val Ser Lys Asp Glu Gln
                    1890               1895               1900

     Tyr Leu Phe Leu Val Arg Val Val Pro Tyr Gln Gly Pro Ser Ser
     1905               1910               1915               1920

     Asp Tyr Val Val Val Lys Met Ile Pro Asp Ser Arg Leu Pro Pro Arg
                    1925               1930               1935

     His Leu His Val Val His Thr Gly Lys Thr Ser Val Val Ile Lys Trp
                    1940               1945               1950

     Glu Ser Pro Tyr Asp Ser Pro Asp Gln Asp Leu Leu Tyr Ala Ile Ala
                    1955               1960               1965

     Val Lys Asp Leu Ile Arg Lys Thr Asp Arg Ser Tyr Lys Val Lys Ser
                    1970               1975               1980

     Arg Asn Ser Thr Val Glu Tyr Thr Leu Asn Lys Leu Glu Pro Gly Gly
     1985               1990               1995               2000
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95

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        Lys Tyr His Ile Ile Val Gln Leu Gly Asn Met Ser Lys Asp Ser Ser
                    2005                    2010              2015

        Ile Lys Ile Thr Thr Val Ser Leu Ser Ala Pro Asp Ala Leu Lys Ile
                    2020                    2025              2030

        Ile Thr Glu Asn Asp His Val Leu Leu Phe Trp Lys Ser Leu Ala Leu
                    2035                    2040              2045

        Lys Glu Lys His Phe Asn Glu Ser Arg Gly Tyr Glu Ile His Met Phe
                    2050                    2055              2060

        Asp Ser Ala Met Asn Ile Thr Ala Tyr Leu Gly Asn Thr Thr Asp Asn
        2065                    2070                    2075              2080

        Phe Phe Lys Ile Ser Asn Leu Lys Met Gly His Asn Tyr Thr Phe Thr
                    2085                    2090              2095

        Val Gln Ala Arg Cys Leu Phe Gly Asn Gln Ile Cys Gly Glu Pro Ala
                    2100                    2105              2110

        Ile Leu Leu Tyr Asp Glu Leu Gly Ser Gly Ala Asp Ala Ser Ala Thr
                    2115                    2120              2125

        Gln Ala Ala Arg Ser Thr Asp Val Ala Ala Val Val Val Pro Ile Leu
                    2130                    2135              2140

        Phe Leu Ile Leu Leu Ser Leu Gly Val Gly Phe Ala Ile Leu Tyr Thr
        2145                    2150                    2155              2160

        Lys His Arg Arg Leu Gln Ser Ser Phe Thr Ala Phe Ala Asn Ser His
                    2165                    2170              2175

        Tyr Ser Ser Arg Leu Gly Ser Ala Ile Phe Ser Ser Gly Asp Asp Leu
                    2180                    2185              2190

        Gly Glu Asp Asp Glu Asp Ala Pro Met Ile Thr Gly Phe Ser Asp Asp
                    2195                    2200              2205

        Val Pro Met Val Ile Ala
                    2210
```

(2) INFORMATION FOR SEQ ID NO: 7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6843 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA to mRNA

    (ix) FEATURE:
        (A) NAME/KEY: sig peptide
        (B) LOCATION:81..164
        (C) IDENTIFICATION METHOD: S

    (ix) FEATURE:
        (A) NAME/KEY: mat peptide
        (B) LOCATION:165..6722
        (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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                                            CCG GCCCAGCGGC TCTCCTGGCC    23
         TCGCGCTGCA CATTCTCTCC TGGCGGCGGC GCCACCTGCA GTAGCGTTCG CCCGAACATG    83
                                                                    Met
                                                                     1
         GCG ACA CGG AGC AGC AGG AGG GAG TCG CGA CTC CCG TTC CTA TTC ACC     131
         Ala Thr Arg Ser Ser Arg Arg Glu Ser Arg Leu Pro Phe Leu Phe Thr
                      5               10                  15
         CTG GTC GCA CTG CTG CCG CCC GGA GCT CTC TGC GAA GTC TGG ACG CAG     179
         Leu Val Ala Leu Leu Pro Pro Gly Ala Leu Cys Glu Val Trp Thr Gln
                      20                  25                  30
         AGG CTG CAC GGC GGC AGC GCG CCC TTG CCC CAG GAC CGG GGC TTC CTC     227
         Arg Leu His Gly Gly Ser Ala Pro Leu Pro Gln Asp Arg Gly Phe Leu
                  35                  40                  45
         GTG GTG CAG GGC GAC CCG CGC GAG CTG CGG CTG TGG GCG CGC GGG GAT     275
         Val Val Gln Gly Asp Pro Arg Glu Leu Arg Leu Trp Ala Arg Gly Asp
         50                  55                  60                  65
         GCC AGG GGG GCG AGC CGC GCG GAC GAG AAG CCG CTC CGG AGG AAA CGG     323
         Ala Arg Gly Ala Ser Arg Ala Asp Glu Lys Pro Leu Arg Arg Lys Arg
                          70                  75                  80
         AGC GCT GCC CTG CAG CCC GAG CCC ATC AAG GTG TAC GGA CAG GTT AGT    ·371
         Ser Ala Ala Leu Gln Pro Glu Pro Ile Lys Val Tyr Gly Gln Val Ser
                      85                  90                  95
         CTG AAT GAT TCC CAC AAT CAG ATG GTG GTG CAC TGG GCT GGA GAG AAA     419
         Leu Asn Asp Ser His Asn Gln Met Val Val His Trp Ala Gly Glu Lys
                      100                 105                 110
         AGC AAC GTG ATC GTG GCC TTG GCC CGA GAT AGC CTG GCA TTG GCG AGG     467
         Ser Asn Val Ile Val Ala Leu Ala Arg Asp Ser Leu Ala Leu Ala Arg
                  115                 120                 125
         CCC AAG AGC AGT GAT GTG TAC GTG TCT TAC GAC TAT GGA AAA TCA TTC     515
         Pro Lys Ser Ser Asp Val Tyr Val Ser Tyr Asp Tyr Gly Lys Ser Phe
         130                 135                 140                 145
         AAG AAA ATT TCA GAC AAG TTA AAC TTT GGC TTG GGA AAT AGG AGT GAA     563
         Lys Lys Ile Ser Asp Lys Leu Asn Phe Gly Leu Gly Asn Arg Ser Glu
                          150                 155                 160
         GCT GTT ATC GCC CAG TTC TAC CAC AGC CCT GCG GAC AAC AAG CGG TAC     611
         Ala Val Ile Ala Gln Phe Tyr His Ser Pro Ala Asp Asn Lys Arg Tyr
                      165                 170                 175
         ATC TTT GCA GAC GCT TAT GCC CAG TAC CTC TGG ATC ACG TTT GAC TTC     659
         Ile Phe Ala Asp Ala Tyr Ala Gln Tyr Leu Trp Ile Thr Phe Asp Phe
                      180                 185                 190
         TGC AAC ACT CTT CAA GGC TTT TCC ATC CCA TTT CGG GCA GCT GAT CTC     707
         Cys Asn Thr Leu Gln Gly Phe Ser Ile Pro Phe Arg Ala Ala Asp Leu
                  195                 200                 205
         CTC CTA CAC AGT AAG GCC TCC AAC CTT CTC TTG GGC TTT GAC AGG TCC     755
         Leu Leu His Ser Lys Ala Ser Asn Leu Leu Leu Gly Phe Asp Arg Ser
         210                 215                 220                 225
         CAC CCC AAC AAG CAG CTG TGG AAG TCA GAT GAC TTT GGC CAG ACC TGG     803
         His Pro Asn Lys Gln Leu Trp Lys Ser Asp Asp Phe Gly Gln Thr Trp
                          230                 235                 240
         ATC ATG ATT CAG GAA CAT GTC AAG TCC TTT TCT TGG GGA ATT GAT CCC     851
         Ile Met Ile Gln Glu His Val Lys Ser Phe Ser Trp Gly Ile Asp Pro
                      245                 250                 255
         TAT GAC AAA CCA AAT ACC ATC TAC ATT GAA CGA CAC GAA CCC TCT GGC     899
         Tyr Asp Lys Pro Asn Thr Ile Tyr Ile Glu Arg His Glu Pro Ser Gly
                      260                 265                 270
         TAC TCC ACT GTC TTC CGA AGT ACA GAT TTC TTC CAG TCC CGG GAA AAC     947
         Tyr Ser Thr Val Phe Arg Ser Thr Asp Phe Phe Gln Ser Arg Glu Asn
         275                 280                 285
         CAG GAA GTG ATC CTT GAG GAA GTG AGA GAT TTT CAG CTT CGG GAC AAG     995
         Gln Glu Val Ile Leu Glu Glu Val Arg Asp Phe Gln Leu Arg Asp Lys
         290                 295                 300                 305
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BNSDOCID: <EP___0773290A2_I_>

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TAC ATG TTT GCT ACA AAG GTG GTG CAT CTC TTG GGC ACT GAA CAC CAG   1043
Tyr Met Phe Ala Thr Lys Val Val His Leu Leu Gly Ser Glu Gln Gln
            310                     315                     320
TCT TCT GTC CAG CTC TGG GTC TCC TTT GGC CGG AAG CCC ATG AGA GCA   1091
Ser Ser Val Gln Leu Trp Val Ser Phe Gly Arg Lys Pro Met Arg Ala
                325                     330                     335
GCC CAG TTT GTC ACA AGA CAT CCT ATT AAT GAA TAT TAC ATC GCA GAT   1139
Ala Gln Phe Val Thr Arg His Pro Ile Asn Glu Tyr Tyr Ile Ala Asp
            340                     345                     350
GCC TCC GAG GAC CAG GTG TTT GTG TGT GTC AGC CAC AGT AAC AAC CGC   1187
Ala Ser Glu Asp Gln Val Phe Val Cys Val Ser His Ser Asn Asn Arg
            355                     360                     365
ACC AAT TTA TAC ATC TCA GAG GCA GAG GGG CTG AAG TTC TCC CTG TCC   1235
Thr Asn Leu Tyr Ile Ser Glu Ala Glu Gly Leu Lys Phe Ser Leu Ser
370                     375                     380                 385
TTG GAG AAC GTG CTC TAT TAC AGC CCA GGA GGG GCC GGC AGT GAC ACC   1283
Leu Glu Asn Val Leu Tyr Tyr Ser Pro Gly Gly Ala Gly Ser Asp Thr
                390                     395                     400
TTG GTG AGG TAT TTT GCA AAT GAA CCA TTT GCT GAC TTC CAC CGA GTG   1331
Leu Val Arg Tyr Phe Ala Asn Glu Pro Phe Ala Asp Phe His Arg Val
            405                     410                     415
GAA GGA TTG CAA GGA GTC TAC ATT GCT ACT CTG ATT AAT GGT TCT ATG   1379
Glu Gly Leu Gln Gly Val Tyr Ile Ala Thr Leu Ile Asn Gly Ser Met
            420                     425                     430
AAT GAG GAG AAC ATG AGA TCG GTC ATC ACC TTT GAC AAA GGG GGA ACC   1427
Asn Glu Glu Asn Met Arg Ser Val Ile Thr Phe Asp Lys Gly Gly Thr
            435                     440                     445
TGG GAG TTT CTT CAG GCT CCA GCC TTC ACG GGA TAT GGA GAG AAA ATC   1475
Trp Glu Phe Leu Gln Ala Pro Ala Phe Thr Gly Tyr Gly Glu Lys Ile
450                     455                     460                 465
AAT TGT GAG CTT TCC CAG GGC TGT TCC CTT CAT CTG GCT CAG CGC CTC   1523
Asn Cys Glu Leu Ser Gln Gly Cys Ser Leu His Leu Ala Gln Arg Leu
                470                     475                     480
AGT CAG CTC CTC AAC CTC CAG CTC CGG AGA ATG CCC ATC CTG TCC AAG   1571
Ser Gln Leu Leu Asn Leu Gln Leu Arg Arg Met Pro Ile Leu Ser Lys
                485                     490                     495
GAG TCG GCT CCA GGC CTC ATC ATC GCC ACT GGC TCA GTG GGA AAG AAC   1619
Glu Ser Ala Pro Gly Leu Ile Ile Ala Thr Gly Ser Val Gly Lys Asn
            500                     505                     510
TTG GCT AGC AAG ACA AAC GTG TAC ATC TCT AGC AGT GCT GGA GCC AGG   1667
Leu Ala Ser Lys Thr Asn Val Tyr Ile Ser Ser Ser Ala Gly Ala Arg
            515                     520                     525
TGG CGA GAG GCA CTT CCT GGA CCT CAC TAC TAC ACA TGG GGA GAC CAC   1715
Trp Arg Glu Ala Leu Pro Gly Pro His Tyr Tyr Thr Trp Gly Asp His
530                     535                     540                 545
GGC GGA ATC ATC ACG GCC ATT GCC CAG GGC ATG GAA ACC AAC GAG CTA   1763
Gly Gly Ile Ile Thr Ala Ile Ala Gln Gly Met Glu Thr Asn Glu Leu
                550                     555                     560
AAA TAC AGT ACC AAT GAA GGG GAG ACC TGG AAA ACA TTC ATC TTC TCT   1811
Lys Tyr Ser Thr Asn Glu Gly Glu Thr Trp Lys Thr Phe Ile Phe Ser
                565                     570                     575
GAG AAG CCA GTG TTT GTG TAT GGC CTC CTC ACA GAA CCT GGG GAG AAG   1859
Glu Lys Pro Val Phe Val Tyr Gly Leu Leu Thr Glu Pro Gly Glu Lys
                580                     585                     590
AGC ACT GTC TTC ACC ATC TTT GGC TCG AAC AAA GAG AAT GTC CAC AGC   1907
Ser Thr Val Phe Thr Ile Phe Gly Ser Asn Lys Glu Asn Val His Ser
            595                     600                     605
TGG CTG ATC CTC CAG GTC AAT GCC ACG GAT GCC TTG GGA GTT CCC TGC   1955
Trp Leu Ile Leu Gln Val Asn Ala Thr Asp Ala Leu Gly Val Pro Cys
610                     615                     620                 625
ACA GAG AAT GAC TAC AAG CTG TGG TCA CCA TCT GAT GAG CGG GGG AAT   2003
Thr Glu Asn Asp Tyr Lys Leu Trp Ser Pro Ser Asp Glu Arg Gly Asn
                630                     635                     640
GAG TGT TTG CTG GGA CAC AAG ACT GTT TTC AAA CGG CGG ACC CCC CAT   2051
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      Glu Cys Leu Leu Gly His Lys Thr Val Phe Lys Arg Arg Thr Pro His
                  645                 650                 655
      GCC ACA TGC TTC AAT GGA GAG GAC TTT GAC AGG CCG GTG GTC GTG TCC      2099
 5    Ala Thr Cys Phe Asn Gly Glu Asp Phe Asp Arg Pro Val Val Val Ser
                  660                 665                 670
      AAC TGC TCC TGC ACC CGG GAG GAC TAT GAG TGT GAC TTC GGT TTC AAG      2147
      Asn Cys Ser Cys Thr Arg Glu Asp Tyr Glu Cys Asp Phe Gly Phe Lys
                  675                 680                 685
      ATG AGT GAA GAT TTG TCA TTA GAG GTT TGT GTT CCA GAT CCG GAA TTT      2195
10    Met Ser Glu Asp Leu Ser Leu Glu Val Cys Val Pro Asp Pro Glu Phe
      690                 695                 700                 705
      TCT GGA AAG TCA TAC TCC CCT CCT GTG CCT TGC CCT GTG GGT TCT ACT      2243
      Ser Gly Lys Ser Tyr Ser Pro Pro Val Pro Cys Pro Val Gly Ser Thr
                  710                 715                 720
      TAC AGG AGA ACG AGA GGC TAC CGG AAG ATT TCT GGG GAC ACT TGT AGC      2291
15    Tyr Arg Arg Thr Arg Gly Tyr Arg Lys Ile Ser Gly Asp Thr Cys Ser
                  725                 730                 735
      GGA GGA GAT GTT GAA GCG CGA CTG GAA GGA GAG CTG GTC CCC TGT CCC      2339
      Gly Gly Asp Val Glu Ala Arg Leu Glu Gly Glu Leu Val Pro Cys Pro
                  740                 745                 750
      CTG GCA GAA GAG AAC GAG TTC ATT CTG TAT GCT GTG AGG AAA TCC ATC      2387
20    Leu Ala Glu Glu Asn Glu Phe Ile Leu Tyr Ala Val Arg Lys Ser Ile
                  755                 760                 765
      TAC CGC TAT GAC CTG GCC TCG GGA GCC ACC GAG CAG TTG CCT CTC ACC      2435
      Tyr Arg Tyr Asp Leu Ala Ser Gly Ala Thr Glu Gln Leu Pro Leu Thr
      770                 775                 780                 785
      GGG CTA CGG GCA GCA GTG GCC CTG GAC TTT GAC TAT GAG CAC AAC TGT      2483
      Gly Leu Arg Ala Ala Val Ala Leu Asp Phe Asp Tyr Glu His Asn Cys
                  790                 795                 800
25    TTG TAT TGG TCC GAC CTG GCC TTG GAC GTC ATC CAG CGC CTC TGT TTG      2531
      Leu Tyr Trp Ser Asp Leu Ala Leu Asp Val Ile Gln Arg Leu Cys Leu
                  805                 810                 815
      AAT GGA AGC ACA GGG CAA GAG GTG ATC ATC AAT TCT GGC CTG GAG ACA      2579
      Asn Gly Ser Thr Gly Gln Glu Val Ile Ile Asn Ser Gly Leu Glu Thr
                  820                 825                 830
30    GTA GAA GCT TTG GCT TTT GAA CCC CTC AGC CAG CTG CTT TAC TGG GTA      2627
      Val Glu Ala Leu Ala Phe Glu Pro Leu Ser Gln Leu Leu Tyr Trp Val
                  835                 840                 845
      GAT GCA GGC TTC AAA AAG ATT GAG GTA GCT AAT CCA GAT GGC GAC TTC      2675
      Asp Ala Gly Phe Lys Lys Ile Glu Val Ala Asn Pro Asp Gly Asp Phe
      850                 855                 860                 865
35    CGA CTC ACA ATC GTC AAT TCC TCT GTG CTT GAT CGT CCC AGG GCT CTG      2723
      Arg Leu Thr Ile Val Asn Ser Ser Val Leu Asp Arg Pro Arg Ala Leu
                  870                 875                 880
      GTC CTC GTG CCC CAA GAG GGG GTG ATG TTC TGG ACA GAC TGG GGA GAC      2771
      Val Leu Val Pro Gln Glu Gly Val Met Phe Trp Thr Asp Trp Gly Asp
                  885                 890                 895
40    CTG AAG CCT GGG ATT TAT CGG AGC AAT ATG GAT GGT TCT GCT GCC TAT      2819
      Leu Lys Pro Gly Ile Tyr Arg Ser Asn Met Asp Gly Ser Ala Ala Tyr
                  900                 905                 910
      CAC CTG GTG TCT GAG GAT GTG AAG TGG CCC AAT GGC ATC TCT GTG GAC      2867
      His Leu Val Ser Glu Asp Val Lys Trp Pro Asn Gly Ile Ser Val Asp
                  915                 920                 925
      GAC CAG TGG ATT TAC TGG ACG GAT GCC TAC CTG GAG TGC ATA GAG CGG      2915
45    Asp Gln Trp Ile Tyr Trp Thr Asp Ala Tyr Leu Glu Cys Ile Glu Arg
      930                 935                 940                 945
      ATC ACG TTC AGT GGC CAG CAG CGC TCT GTC ATT CTG GAC AAC CTC CCG      2963
      Ile Thr Phe Ser Gly Gln Gln Arg Ser Val Ile Leu Asp Asn Leu Pro
                  950                 955                 960
      CAC CCC TAT GCC ATT GCT GTC TTT AAG AAT GAA ATC TAC TGG GAT GAC      3011
50    His Pro Tyr Ala Ile Ala Val Phe Lys Asn Glu Ile Tyr Trp Asp Asp
                  965                 970                 975
      TGG TCA CAG CTC AGC ATA TTC CGA GCT TCC AAA TAC AGT GGG TCC CAG      3059
      Trp Ser Gln Leu Ser Ile Phe Arg Ala Ser Lys Tyr Ser Gly Ser Gln

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                980                        985                     940
        ATG GAG ATT CTG GCA AAC CAG CTC ACG GGG CTC ATG GAC ATG AAG ATT    3107
        Met Glu Ile Leu Ala Asn Gln Leu Thr Gly Leu Met Asp Met Lys Ile
            995                       1000                    1005
        TTC TAC AAG GGG AAG AAC ACT GGA AGC AAT GCC TGT GTG CCC AGG CCA    3155
        Phe Tyr Lys Gly Lys Asn Thr Gly Ser Asn Ala Cys Val Pro Arg Pro
        1010                      1015                    1020        1025
        TGC AGC CTG CTG TGC CTG CCC AAG GCC AAC AAC AGT AGA AGC TGC AGG    3203
        Cys Ser Leu Leu Cys Leu Pro Lys Ala Asn Asn Ser Arg Ser Cys Arg
                        1030                    1035                1040
        TGT CCA GAG GAT GTG TCC AGC AGT GTG CTT CCA TCA GGG GAC CTG ATG    3251
        Cys Pro Glu Asp Val Ser Ser Ser Val Leu Pro Ser Gly Asp Leu Met
                    1045                    1050                1055
        TGT GAC TGC CCT CAG GGC TAT CAG CTC AAG AAC AAT ACC TGT GTC AAA    3299
        Cys Asp Cys Pro Gln Gly Tyr Gln Leu Lys Asn Asn Thr Cys Val Lys
                    1060                    1065                1070
        GAA GAG AAC ACC TGT CTT CGC AAC CAG TAT CGC TGC AGC AAC GGG AAC    3347
        Glu Glu Asn Thr Cys Leu Arg Asn Gln Tyr Arg Cys Ser Asn Gly Asn
                    1075                    1080                1085
        TGT ATC AAC AGC ATT TGG TGG TGT GAC TTT GAC AAC GAC TGT GGA GAC    3395
        Cys Ile Asn Ser Ile Trp Trp Cys Asp Phe Asp Asn Asp Cys Gly Asp
        1090                      1095                    1100        1105
        ATG AGC GAT GAG AGA AAC TGC CCT ACC ACC ATC TGT GAC CTG GAC ACC    3443
        Met Ser Asp Glu Arg Asn Cys Pro Thr Thr Ile Cys Asp Leu Asp Thr
                        1110                    1115                1120
        CAG TTT CGT TGC CAG GAG TCT GGG ACT TGT ATC CCA CTG TCC TAT AAA    3491
        Gln Phe Arg Cys Gln Glu Ser Gly Thr Cys Ile Pro Leu Ser Tyr Lys
                            1125                    1130                1135
        TGT GAC CTT GAG GAT GAC TGT GGA GAC AAC AGT GAT GAA AGT CAT TGT    3539
        Cys Asp Leu Glu Asp Asp Cys Gly Asp Asn Ser Asp Glu Ser His Cys
                    1140                    1145                1150
        GAA ATG CAC CAG TGC CGG AGT GAC GAG TAC AAC TGC AGT TCC GGC ATG    3587
        Glu Met His Gln Cys Arg Ser Asp Glu Tyr Asn Cys Ser Ser Gly Met
                    1155                    1160                1165
        TGC ATC CGC TCC TCC TGG GTA TGT GAC GGG GAC AAC GAC TGC AGG GAC    3635
        Cys Ile Arg Ser Ser Trp Val Cys Asp Gly Asp Asn Asp Cys Arg Asp
        1170                      1175                    1180        1185
        TGG TCT GAT GAA GCC AAC TGT ACC GCC ATC TAT CAC ACC TGT GAG GCC    3683
        Trp Ser Asp Glu Ala Asn Cys Thr Ala Ile Tyr His Thr Cys Glu Ala
                        1190                    1195                1200
        TCC AAC TTC CAG TGC CGA AAC GGG CAC TGC ATC CCC CAG CGG TGG GCG    3731
        Ser Asn Phe Gln Cys Arg Asn Gly His Cys Ile Pro Gln Arg Trp Ala
                        1205                    1210                1215
        TGT GAC GGG GAT ACG GAC TGC CAG GAT GGT TCC GAT GAG GAT CCA GTC    3779
        Cys Asp Gly Asp Thr Asp Cys Gln Asp Gly Ser Asp Glu Asp Pro Val
                    1220                    1225                1230
        AAC TGT GAG AAG AAG TGC AAT GGA TTC CGC TGC CCA AAC GGC ACT TGC    3827
        Asn Cys Glu Lys Lys Cys Asn Gly Phe Arg Cys Pro Asn Gly Thr Cys
                    1235                    1240                1245
        ATC CCA TCC AGC AAA CAT TGT GAT GGT CTG CGT GAT TGC TCT GAT GGC    3875
        Ile Pro Ser Ser Lys His Cys Asp Gly Leu Arg Asp Cys Ser Asp Gly
        1250                      1255                    1260        1265
        TCC GAT GAA CAG CAC TGC GAG CCC CTC TGT ACG CAC TTC ATG GAC TTT    3923
        Ser Asp Glu Gln His Cys Glu Pro Leu Cys Thr His Phe Met Asp Phe
                        1270                    1275                1280
        GTG TGT AAG AAC CGC CAG CAG TGC CTG TTC CAC TCC ATG GTC TGT GAC    3971
        Val Cys Lys Asn Arg Gln Gln Cys Leu Phe His Ser Met Val Cys Asp
                    1285                    1290                1295
        GGA ATC ATC CAG TGC CGC GAC GGG TCC GAT GAG GAT GCG GCG TTT GCA    4019
        Gly Ile Ile Gln Cys Arg Asp Gly Ser Asp Glu Asp Ala Ala Phe Ala
                    1300                    1305                1310
        GGA TGC TCC CAA GAT CCT GAG TTC CAC AAG GTA TGT GAT GAG TTC GGT    4067
        Gly Cys Ser Gln Asp Pro Glu Phe His Lys Val Cys Asp Glu Phe Gly
                    1315                    1320                1325
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TTC CAG TGT CAG AAT GGA GTG TGC ATC AGT TTG ATT TGG AAG TGC GAC    4115
Phe Gln Cys Gln Asn Gly Val Cys Ile Ser Leu Ile Trp Lys Cys Asp
1330                    1335                    1340            1345
GGG ATG GAT GAT TGC GGC GAT TAT TCT GAT GAA GCC AAC TGC GAA AAC    4163
Gly Met Asp Asp Cys Gly Asp Tyr Ser Asp Glu Ala Asn Cys Glu Asn
                1350                    1355                    1360
CCC ACA GAA GCC CCA AAC TGC TCC CGC TAC TTC CAG TTT CGG TGT GAG    4211
Pro Thr Glu Ala Pro Asn Cys Ser Arg Tyr Phe Gln Phe Arg Cys Glu
                1365                    1370                    1375
AAT GGC CAC TGC ATC CCC AAC AGA TGG AAA TGT GAC AGG GAG AAC GAC    4259
Asn Gly His Cys Ile Pro Asn Arg Trp Lys Cys Asp Arg Glu Asn Asp
            1380                    1385                    1390
TGT GGG GAC TGG TCT GAT GAG AAG GAT TGT GGA GAT TCA CAT ATT CTT    4307
Cys Gly Asp Trp Ser Asp Glu Lys Asp Cys Gly Asp Ser His Ile Leu
        1395                    1400                    1405
CCC TTC TCG ACT CCT GGG CCC TCC ACG TGT CTG CCC AAT TAC TAC CGC    4355
Pro Phe Ser Thr Pro Gly Pro Ser Thr Cys Leu Pro Asn Tyr Tyr Arg
1410                    1415                    1420                1425
TGC AGC AGT GGG ACC TGC GTG ATG GAC ACC TGG GTG TGC GAC GGG TAC    4403
Cys Ser Ser Gly Thr Cys Val Met Asp Thr Trp Val Cys Asp Gly Tyr
                1430                    1435                    1440
CGA GAT TGT GCA GAT GGC TCT GAC GAG GAA GCC TGC CCC TTG CTT GCA    4451
Arg Asp Cys Ala Asp Gly Ser Asp Glu Glu Ala Cys Pro Leu Leu Ala
                1445                    1450                    1455
AAC GTC ACT GCT GCC TCC ACT CCC ACC CAA CTT GGG CGA TGT GAC CGA    4499
Asn Val Thr Ala Ala Ser Thr Pro Thr Gln Leu Gly Arg Cys Asp Arg
            1460                    1465                    1470
TTT GAG TTC GAA TGC CAC CAA CCG AAG ACG TGT ATT CCC AAC TGG AAG    4547
Phe Glu Phe Glu Cys His Gln Pro Lys Thr Cys Ile Pro Asn Trp Lys
        1475                    1480                    1485
CGC TGT GAC GGC CAC CAA GAT TGC CAG GAT GGC CGG GAC GAG GCC AAT    4595
Arg Cys Asp Gly His Gln Asp Cys Gln Asp Gly Arg Asp Glu Ala Asn
1490                    1495                    1500                1505
TGC CCC ACA CAC AGC ACC TTG ACT TGC ATG AGC AGG GAG TTC CAG TGC    4643
Cys Pro Thr His Ser Thr Leu Thr Cys Met Ser Arg Glu Phe Gln Cys
                1510                    1515                    1520
GAG GAC GGG GAG GCC TGC ATT GTG CTC TCG GAG CGC TGC GAC GGC TTC    4691
Glu Asp Gly Glu Ala Cys Ile Val Leu Ser Glu Arg Cys Asp Gly Phe
                1525                    1530                    1535
CTG GAC TGC TCG GAC GAG AGC GAT GAA AAG GCC TGC AGT GAT GAG TTG    4739
Leu Asp Cys Ser Asp Glu Ser Asp Glu Lys Ala Cys Ser Asp Glu Leu
            1540                    1545                    1550
ACT GTG TAC AAA GTA CAG AAT CTT CAG TGG ACA GCT GAC TTC TCT GGG    4787
Thr Val Tyr Lys Val Gln Asn Leu Gln Trp Thr Ala Asp Phe Ser Gly
        1555                    1560                    1565
GAT GTG ACT TTG ACC TGG ATG AGG CCC AAA AAA ATG CCC TCT GCA TCT    4835
Asp Val Thr Leu Thr Trp Met Arg Pro Lys Lys Met Pro Ser Ala Ser
1570                    1575                    1580                1585
TGT GTA TAT AAT GTC TAC TAC AGG GTG GTT GGA GAG AGC ATA TGG AAG    4883
Cys Val Tyr Asn Val Tyr Tyr Arg Val Val Gly Glu Ser Ile Trp Lys
                1590                    1595                    1600
ACT CTG GAG ACC CAC AGC AAT AAG ACA AAC ACT GTA TTA AAA GTC TTG    4931
Thr Leu Glu Thr His Ser Asn Lys Thr Asn Thr Val Leu Lys Val Leu
            1605                    1610                    1615
AAA CCA GAT ACC ACG TAT CAG GTT AAA GTA CAG GTT CAG TGT CTC AGC    4979
Lys Pro Asp Thr Thr Tyr Gln Val Lys Val Gln Val Gln Cys Leu Ser
            1620                    1625                    1630
AAG GCA CAC AAC ACC AAT GAC TTT GTG ACC CTG AGG ACC CCA GAG GGA    5027
Lys Ala His Asn Thr Asn Asp Phe Val Thr Leu Arg Thr Pro Glu Gly
        1635                    1640                    1645
TTG CCA GAT GCC CCT CGA AAT CTC CAG CTG TCA CTC CCC AGG GAA GCA    5075
Leu Pro Asp Ala Pro Arg Asn Leu Gln Leu Ser Leu Pro Arg Glu Ala
1650                    1655                    1660                1665
GAA GGT GTG ATT GTA GGC CAC TGG GCT CCT CCC ATC CAC ACC CAT GGC    5123
Glu Gly Val Ile Val Gly His Trp Ala Pro Pro Ile His Thr His Gly
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Glu Gly Val Ile Val Gly His Trp Ala Pro Pro Ile His Thr His Gly
            1670                    1675              1680
CTC ATC CGT GAG TAC ATT GTA GAA TAC AGC AGG AGT GGT TCC AAG ATG    5171
Leu Ile Arg Glu Tyr Ile Val Glu Tyr Ser Arg Ser Gly Ser Lys Met
            1685                    1690              1695
TGG GCC TCC CAG AGG GCT GCT AGT AAC TTT ACA GAA ATC AAG AAC TTA    5219
Trp Ala Ser Gln Arg Ala Ala Ser Asn Phe Thr Glu Ile Lys Asn Leu
            1700                    1705              1710
TTG GTC AAC ACT CTA TAC ACC GTC AGA GTG GCT GCG GTG ACT AGT CGT    5267
Leu Val Asn Thr Leu Tyr Thr Val Arg Val Ala Ala Val Thr Ser Arg
    1715                    1720                    1725
GGA ATA GGA AAC TGG AGC GAT TCT AAA TCC ATT ACC ACC ATA AAA GGA    5315
Gly Ile Gly Asn Trp Ser Asp Ser Lys Ser Ile Thr Thr Ile Lys Gly
1730                    1735                    1740              1745
AAA GTG ATC CCA CCA CCA GAT ATC CAC ATT GAC AGC TAT GGT GAA AAT    5363
Lys Val Ile Pro Pro Pro Asp Ile His Ile Asp Ser Tyr Gly Glu Asn
                    1750                    1755              1760
TAT CTA AGC TTC ACC CTG ACC ATG GAG AGT GAT ATC AAG GTG AAT GGC    5411
Tyr Leu Ser Phe Thr Leu Thr Met Glu Ser Asp Ile Lys Val Asn Gly
                1765                    1770              1775
TAT GTG GTG AAC CTT TTC TGG GCA TTT GAC ACC CAC AAG CAA GAG AGG    5459
Tyr Val Val Asn Leu Phe Trp Ala Phe Asp Thr His Lys Gln Glu Arg
    1780                    1785                    1790
AGA ACT TTG AAC TTC CGA GGA AGC ATA TTG TCA CAC AAA GTT GGC AAT    5507
Arg Thr Leu Asn Phe Arg Gly Ser Ile Leu Ser His Lys Val Gly Asn
    1795                    1800                    1805
CTG ACA GCT CAT ACA TCC TAT GAG ATT TCT GCC TGG GCC AAG ACT GAC    5555
Leu Thr Ala His Thr Ser Tyr Glu Ile Ser Ala Trp Ala Lys Thr Asp
1810                    1815                    1820              1825
TTG GGG GAT AGC CCT CTG GCA TTT GAG CAT GTT ATG ACC AGA GGG GTT    5603
Leu Gly Asp Ser Pro Leu Ala Phe Glu His Val Met Thr Arg Gly Val
                1830                    1835              1840
CGC CCA CCT GCA CCT AGC CTC AAG GCC AAA GCC ATC AAC CAG ACT GCA    5651
Arg Pro Pro Ala Pro Ser Leu Lys Ala Lys Ala Ile Asn Gln Thr Ala
            1845                    1850              1855
GTG GAA TGT ACC TGG ACC GGC CCC CGG AAT GTG GTT TAT GGT ATT TTC    5699
Val Glu Cys Thr Trp Thr Gly Pro Arg Asn Val Val Tyr Gly Ile Phe
            1860                    1865              1870
TAT GCC ACG TCC TTT CTT GAC CTC TAT CGC AAC CCG AAG AGC TTG ACT    5747
Tyr Ala Thr Ser Phe Leu Asp Leu Tyr Arg Asn Pro Lys Ser Leu Thr
    1875                    1880                    1885
ACT TCA CTC CAC AAC AAG ACG GTC ATT GTC AGT AAG GAT GAG CAG TAT    5795
Thr Ser Leu His Asn Lys Thr Val Ile Val Ser Lys Asp Glu Gln Tyr
1890                    1895                    1900              1905
TTG TTT CTG GTC CGT GTA GTG GTA CCC TAC CAG GGG CCA TCC TCT GAC    5843
Leu Phe Leu Val Arg Val Val Val Pro Tyr Gln Gly Pro Ser Ser Asp
                1910                    1915              1920
TAC GTT GTA GTG AAG ATG ATC CCG GAC AGC AGG CTT CCA CCC CGT CAC    5891
Tyr Val Val Val Lys Met Ile Pro Asp Ser Arg Leu Pro Pro Arg His
                1925                    1930              1935
CTG CAT GTG GTT CAT ACG GGC AAA ACC TCC GTG GTC ATC AAG TGG GAA    5939
Leu His Val Val His Thr Gly Lys Thr Ser Val Val Ile Lys Trp Glu
1940                    1945                    1950
TCA CCG TAT GAC TCT CCT GAC CAG GAC TTG TTG TAT GCA ATT GCA GTC    5987
Ser Pro Tyr Asp Ser Pro Asp Gln Asp Leu Leu Tyr Ala Ile Ala Val
    1955                    1960                    1965
AAA GAT CTC ATA AGA AAG ACT GAC AGG AGC TAC AAA GTA AAA TCC CGT    6035
Lys Asp Leu Ile Arg Lys Thr Asp Arg Ser Tyr Lys Val Lys Ser Arg
1970                    1975                    1980              1985
AAC AGC ACT GTG GAA TAC ACC CTT AAC AAG TTG GAG CCT GGC GGG AAA    6083
Asn Ser Thr Val Glu Tyr Thr Leu Asn Lys Leu Glu Pro Gly Gly Lys
                1990                    1995              2000
TAC CAC ATC ATT GTC CAA CTG GGG AAC ATG AGC AAA GAT TCC AGC ATA    6131
Tyr His Ile Ile Val Gln Leu Gly Asn Met Ser Lys Asp Ser Ser Ile
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                    2005                    2010                    2015
        AAA ATT ACC ACA GTT TCA TTA TCA GCA CCT GAT GCC TTA AAA ATC ATA   6179
        Lys Ile Thr Thr Val Ser Leu Ser Ala Pro Asp Ala Leu Lys Ile Ile
                    2020                    2025                    2030
        ACA GAA AAT GAT CAT GTT CTT CTG TTT TGG AAA AGC CTG GCT TTA AAG   6227
        Thr Glu Asn Asp His Val Leu Leu Phe Trp Lys Ser Leu Ala Leu Lys
                    2035                    2040                    2045
        GAA AAG CAT TTT AAT GAA AGC AGG GGC TAT GAG ATA CAC ATG TTT GAT   6275
        Glu Lys His Phe Asn Glu Ser Arg Gly Tyr Glu Ile His Met Phe Asp
        2050                    2055                    2060           2065
        AGT GCC ATG AAT ATC ACA GCT TAC CTT GGG AAT ACT ACT GAC AAT TTC   6323
        Ser Ala Met Asn Ile Thr Ala Tyr Leu Gly Asn Thr Thr Asp Asn Phe
                    2070                    2075                    2080
        TTT AAA ATT TCC AAC CTG AAG ATG GGT CAT AAT TAC ACG TTC ACC GTC   6371
        Phe Lys Ile Ser Asn Leu Lys Met Gly His Asn Tyr Thr Phe Thr Val
                    2085                    2090                    2095
        CAA GCA AGA TGC CTT TTT GGC AAC CAG ATC TGT GGG GAG CCT GCC ATC   6419
        Gln Ala Arg Cys Leu Phe Gly Asn Gln Ile Cys Gly Glu Pro Ala Ile
                    2100                    2105                    2110
        CTG CTG TAC GAT GAG CTG GGG TCT GGT GCA GAT GCA TCT GCA ACG CAG   6467
        Leu Leu Tyr Asp Glu Leu Gly Ser Gly Ala Asp Ala Ser Ala Thr Gln
                    2115                    2120                    2125
        GCT GCC AGA TCT ACG GAT GTT GCT GCT GTG GTG GTG CCC ATC TTA TTC   6515
        Ala Ala Arg Ser Thr Asp Val Ala Ala Val Val Val Pro Ile Leu Phe
        2130                    2135                    2140           2145
        CTG ATA CTG CTG AGC CTG GGG GTG GGG TTT GCC ATC CTG TAC ACG AAG   6563
        Leu Ile Leu Leu Ser Leu Gly Val Gly Phe Ala Ile Leu Tyr Thr Lys
                    2150                    2155                    2160
        CAC CGG AGG CTG CAG AGC AGC TTC ACC GCC TTC GCC AAC AGC CAC TAC   6611
        His Arg Arg Leu Gln Ser Ser Phe Thr Ala Phe Ala Asn Ser His Tyr
                    2165                    2170                    2175
        AGC TCC AGG CTG GGG TCC GCA ATC TTC TCC TCT GGG GAT GAC CTG GGG   6659
        Ser Ser Arg Leu Gly Ser Ala Ile Phe Ser Ser Gly Asp Asp Leu Gly
                    2180                    2185                    2190
        GAA GAT GAT GAA GAT GCC CCT ATG ATA ACT GGA TTT TCA GAT GAC GTC   6707
        Glu Asp Asp Glu Asp Ala Pro Met Ile Thr Gly Phe Ser Asp Asp Val
                    2195                    2200                    2205
        CCC ATG GTG ATA GCC TGAAAGAGCT TTCCTCACTA GAAACCAAAT GGTGTAAATA   6762
        Pro Met Val Ile Ala
        2210
        TTTTATTTGA TAAAGATAGT TGATGGTTTA TTTTAAAAGA TGCACTTTGA GTTGCAATAT   6822
        GTTATTTTTA TATGGGCCAA A                                           6843
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Claims

1. DNA having a nucleotide sequence as shown by Sequence ID No. 1.

2. An LDL receptor analog protein having an amino acid sequence as shown by Sequence ID No. 2 and coded by the DNA of Claim 1.

3. DNA having a nucleotide sequence as shown by Sequence ID No. 5.

4. An LDL receptor analog protein having an amino acid sequence as shown by Sequence ID No. 6 and coded by the DNA of Claim 3.

5. A recombinant vector comprising DNA as shown by Sequence ID No. 1 or 5 and a replicable vector.

6. Transformant cells which harbor the recombinant vector of Claim 5.

7. A method for the production of an LDL receptor analog protein comprising the steps of culturing the transformants of Claim 6 and collecting a polypeptide produced in the culture.

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(12) **EUROPEAN PATENT APPLICATION**

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(54) **Novel LDL receptor analog protein and the gene coding therefor**

(57) The present invention is drawn to the gene of a novel LDL receptor family receptor which participates in lipoprotein metabolism, a critical factor that triggers the onset of arteriosclerosis.

The invention provides DNA having a nucleotide sequence as shown by Sequence ID No. 1 or No.5 is disclosed as well as rabbit tissue or human tissue LDL receptor analog protein having an amino acid sequence of Sequence ID No. 2 or 6 coded by such DNA.

EP 0 773 290 A3

))) European Patent Office

EUROPEAN SEARCH REPORT

Application Number

EP 96 11 6108

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
A	WO 94 10322 A (UNIVERSITY OF TEXAS) * the whole document * ---	1-7	C12N15/12 C07K14/705 //C12N15/70, C12N15/79
A	WO 95 13374 A (BAYLOR COLLEGE OF MEDICINE) * the whole document * ---	1-7	
A	KOZARSKY K. ET AL.: "In vivo correction of low density lipoprotein receptor deficiency in the Watanabe heritable hyperlipemic rabbit with recombinant adenoviruses" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 269, no. 18, 6 May 1994, MD US, pages 13695-13702, XP002062181 * the whole document * ---	1-7	
A	WILSON J.M. ET AL.: "Hepathocyte-directed gene transfer in vivo leads to transient improvement of hypercholesterolemia in low density lipoprotein receptor-deficient rabbits" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 267, no. 2, 15 January 1995, MD US, pages 963-967, XP002062183 * the whole document * -----	1-7	TECHNICAL FIELDS SEARCHED (Int.Cl.6) C07K

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
BERLIN	16 April 1998	Panzica, G

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another
     document of the same category
A : technological background
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P : intermediate document

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E : earlier patent document, but published on, or
     after the filing date
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     document